

Figure 1

Fatty Acid Biosynthesis Pathways

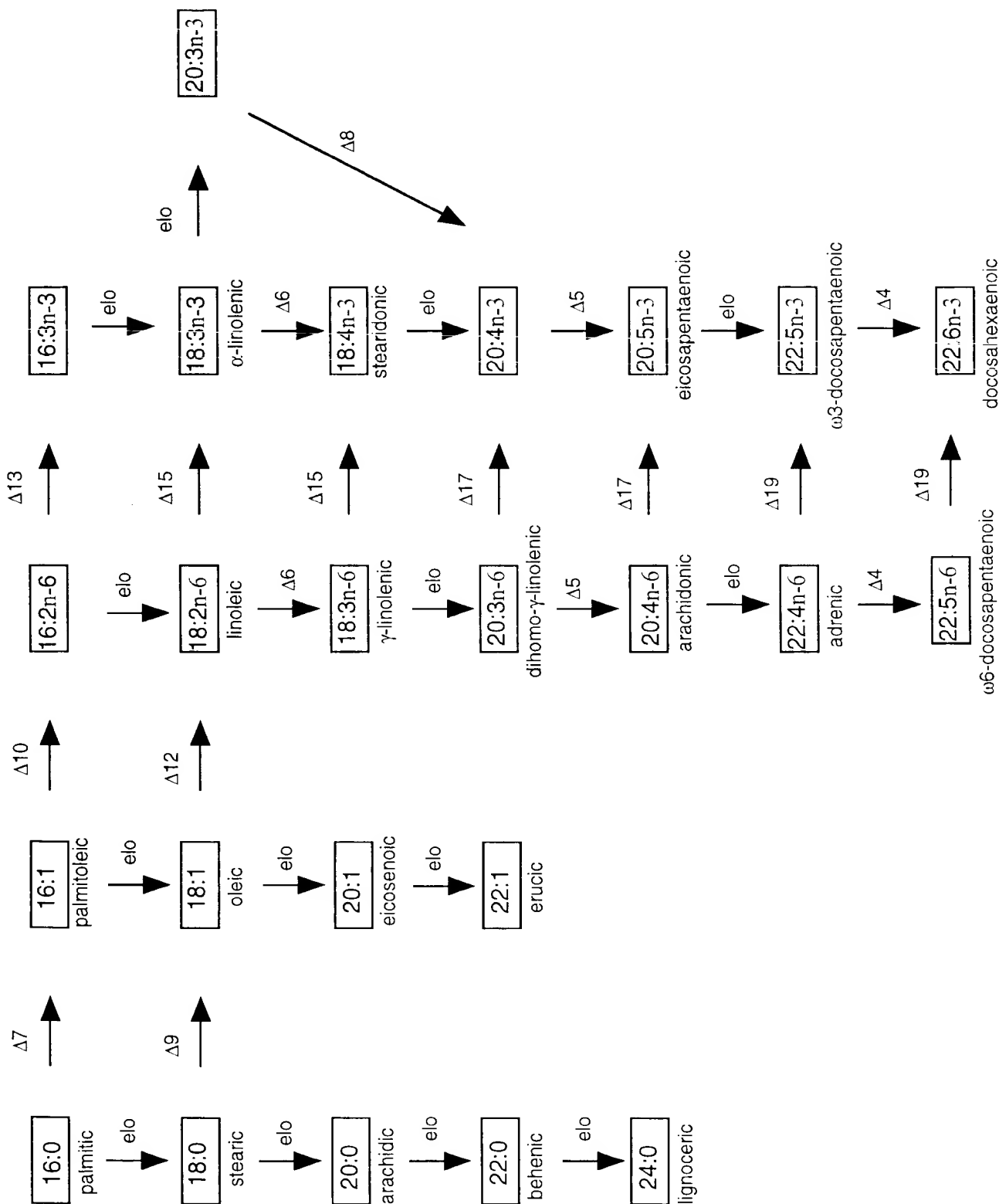


Figure 2

Gap Weight: 6 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003
Quality: 50 Length: 84
Ratio: 0.625 Gaps: 4
Percent Similarity: 43.038 Percent Identity: 29.114

Match display thresholds for the alignment(s):

| = IDENTITY

: = 2

. = 1

jojobakcs x ELO2

June 4, 1998 08:23 ..

jojobakcs 24 ATLPNFKSSINLHHVKL.GYHYLISNALFLVFIPLLGLASAHLSFSFSAHD 72
 .|.|. .| :.| :| :|:|. | | | | | ..
ELO2 66 STLPPVLYAITAYYVIIFGGRFLLSKS..KPF.KLNGLFQLHNLVLTSL 112

jojobakcs 73 LSLLFDLLRRNLLPVVCSFLFVLLATLHFLTRP 106
 |.|| |:|. |:| : : :|. |
ELO2 113 LTLLL.LMVEQLVPIIVQHGLYFAICNIGAWTQP 145

Figure 3

S. cerevisiae ELO2 (AA66-145) with *M. alpina* codon bias

S	T	L	P	P	V	L	Y	A	I	T	A	Y	Y	V	I	I	F	G	G	R	F	L
66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88
TCC	ACC	CTC	CCC	CCC	GTC	CTC	TAC	GCC	ATC	ACC	GCC	TAC	TAC	GTC	ATC	ATC	TTC	GGT	GGT	CGC	TTC	CTC

<-- R0339

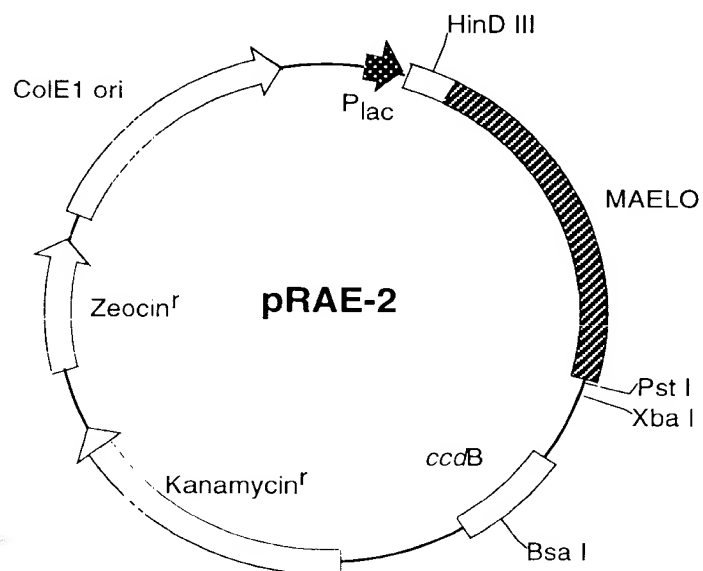
L	S	K	S	K	P	F	K	L	N	G	L	F	Q	L	H	N	L	V	L	T	S	L
89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111
CTC	TCC	AAG	TCC	AAG	CCC	TTC	AAG	CTC	AAC	GGT	CTC	TTC	CAG	CTC	CAC	AAC	CTC	GTC	CTC	ACC	TCC	CTC

S	L	T	L	L	L	L	M	V	E	Q	L	V	P	I	I	V	Q	H	G	L	Y	F
112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134
TCC	CTC	ACC	CTC	CTC	CTC	CTC	ATG	GTC	GAG	CAG	CTC	GTC	CCC	ATC	ATC	GTC	CAG	CAC	GGT	CTC	TAC	TTC

A	I	C	N	I	G	A	W	T	Q	P
135	136	137	138	139	140	141	142	143	144	145
GCC	ATC	TGC	AAC	ATC	GGT	GCC	TGG	ACC	CAG	CCC

Figure 4

A



B

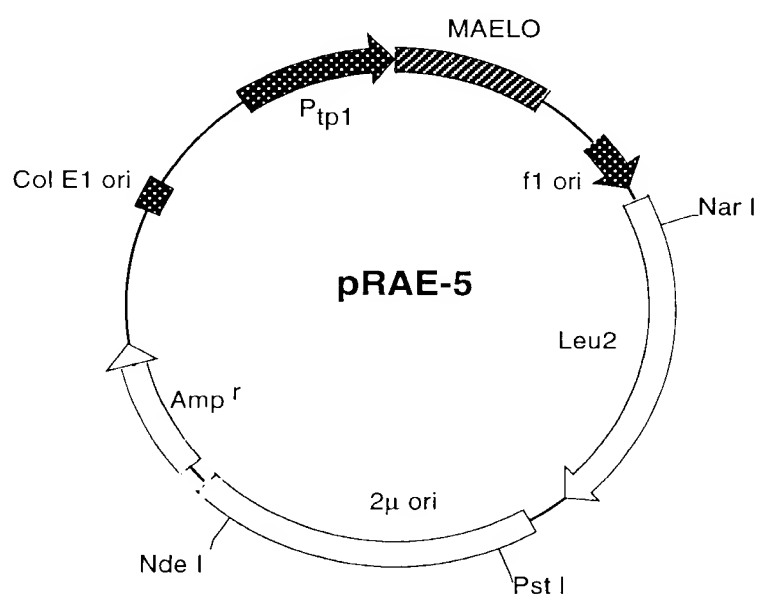


Figure 5

PRAE-5 GAATTCAGG * * * * * CATGGCCCGCCGCAATCTTGACAA
PRAE-6 GAATTCAGGCATCTCATGGATCCGCCCATGGCCCGCCGCAATCTTGACAA
EcoRI BamHI NcoI

Figure 6

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1  ATGGCCGCCG CAATCTTGGA CAAGGTCAAC TTCGGCATTG ATCAGCCCTT
51  CGGAATCAAG CTCGACACCT ACTTTGCTCA GGCTATGAA CTCGTCACCG
101 GAAAGTCCAT CGACTCCTTC GTCTTCCAGG AGGGCGTCAC GCCTCTCTCG
151 ACCCAGAGAG AGGTCGCCAT GTGGACTATC ACTTACTTCG TCGTCATCTT
201 TGGTGGTCGC CAGATCATGA AGAGCCAGGA CGCCTTCAAG CTCAAGCCCC
251 TCTTCATCCT CCACAACCTC CTCCTGACGA TCGCGTCCGG ATCGCTGTTG
301 CTCCTGTTCA TCGAGAACCT GGTCCCCATC CTCGCCAGAA ACGGACTTTT
351 CTACGCCATC TGGGACGACG GTGCCCTGGAC CCAGCGCCTC GAGCTCCTCT
401 ACTACCTCAA CTACCTGGTC AAGTACTGGG AGTTGGCCGA CACCGTCTTT
451 TTGGTCCTCA AGAAGAAGCC TCTTGAGTTC CTGCACTACT TCCACCACTC
501 GATGACCATG GTTCTCTGCT TTGTCCAGCT TGGAGGATAC ACTTCACCTG
551 CCTGGGTCCC TATTACCCTC AACTTGACTC TCCACGTCTT CATGTACTAC
601 TACTACATGC GCTCCGCTGC CGGTGTTTCGC ATCTGGTGGA AGCAGTACTT
651 GACCACTCTC CAGATCGTCC AGTTCGTTCT TGACCTCGGA TTCATCTACT
701 TCTGCGCCTA CACCTACTTC GCCTTCACCT ACTTCCCCTG GGCTCCCAAC
751 GTCGGCAAGT GCGCCGCTAC CGAGGGTGCT GCTCTCTTTG GCTGCGGACT
801 CCTCTCCAGC TATCTCTTGC TCTTTATCAA CTTCTACCGC ATTACCTACA
851 ATGCCAAGGC CAAGGCAGCC AAGGAGCGTG GAAGCAACTT TACCCCCAAG
901 ACTGTCAAGT CCGGCGGATC GCCCAAGAAG CCCTCCAAGA GCAAGCACAT
951 CTAA

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Figure 7

1 MAAAILDKVN FGIDQPFGIK LDTYFAQAYE LVTGKSIDSF VFQEGVTPLS
51 TQREVAMWTI TYFVVIFGGR QIMKSQDAFK LKPLFILHNF LLTIASGSLL
101 LLFIENLVPI LARNGLFYAT CDDGAWTQRL ELLYYLNYLV KYWELADTVF
151 LVLKKKPLEF LHYFHHSMTM VLCFVQLGGY TSVSWVPITL NLTVHVFMYY
201 YYMRSAGVR IWWKQYLTTL QIVQFVLDLG FTYFCAYTYF AFTYFPWAPN
251 VGKCAGTEGA ALFGCGLLSS YLLLFINFYR ITYNAKAKAA KERGSNFTPK
301 TVKSGGSPKK PSKSKHI*

Figure 8

	1	~ ~ ~ ~ ~	M N S L V T Q Y A A P L F E R Y P Q L H D Y L P T L E R P F F N I S L W E H F E D V	50
GNS1	~ ~ ~ ~ ~	~ ~ ~ ~ ~	~ ~ ~ ~ ~	
SUR4	M N T T S T V I A A V A D Q F Q S L N S S S C F L K V H V P S I E N P F . G I E L W P I F S K V			
MAELO	~ ~ ~ ~ ~	~ ~ ~ ~ ~	~ ~ ~ ~ ~	
	51			
GNS1	V T R V T N G R F V P S E F F Q F I A G E L P L S T L P P V L Y A I T A Y Y V I I F G G R F L S K S	100		
SUR4	F E Y F S I . G Y P A E Q I . F E F I H N K T F L A N G Y H A V S I I I V Y Y I I F G G Q A I L R A L			
MAELO	Y E L V T . G K S I D S . F V F Q E G V T P L S T Q R E V A M W T I T Y F V V I F G G R Q I M K S Q			
	101			
GNS1	K P . F K L N G L F E Q L H N L V L T S L S L L L L M V E Q L V P I I V Q H G L Y F A T C N I G	150		
SUR4	N A S P L K F K L L F E I H N L F L T S I S L V L W L M L E Q L V P M W Y H N G L F W S I C S K E			
MAELO	D A . F K L K P L F I L H N F L L T I A S G S L L L L F I E N L V P I L A R N G L F Y A I C D D G			
	151			
GNS1	A W T Q P L V T L Y Y M N Y I V K F I E F I D T F F L V L K H K K L T F L H T Y H H G A T A L L C Y	200		
SUR4	A F A P K L V T L Y Y L N Y L T K F V E L I D T V F L V L R K K L L F L H T Y H H G A T A L L C Y			
MAELO	A W T Q R L E L L Y Y L N Y L V K Y W E L A D T V F L V L K K K P L E F L H Y F H S M T M V L C F			
	201			
GNS1	T Q L M G T S T S I S W V P I S L N L G V H V V M Y W Y Y F L A A R G I R V W W K E W V T R F Q I I I Q	250		
SUR4	T Q L I G R T S V E W V V I L L N L G V H V I M Y W Y Y E L S S I C G I R V W W K Q W V T R F Q I I I Q			
MAELO	V Q L G G Y T S V S W V P I T L N L T V H V F M Y Y Y M R S A A G V R I W W K Q Y L T L L Q I V Q			
	251			
GNS1	F V L D I G F I Y F A V Y O K A V H L Y F P I L . P H C G G D C V G S T T A T H A G G A I I S S Y L V	300		
SUR4	F L I D L V F V Y F A T Y T F Y A H K Y L D G I L P N K G T C Y G T Q A A A A Y G Y L I L T S Y L L			
MAELO	F V L D L G F I Y F C A Y T Y F A F T Y F P W A . P N V G K C A G T E G A A L F G C G L L S S Y L L			
	301			
GNS1	L F I S F Y I N V Y K R K G T K T S R V V K R A H G G V A A K V N E Y V N V D L K N V P T P S P S P	350		
SUR4	L F I S F Y I Q S Y K K G K K T V K K E S E V S I G . S V A S G S S T G V K I S N T K V S S R K A ~			
MAELO	L F I N F Y R I T Y N A K A K A K A K E R G S N F T P K T V K S G G S P K . K P S K S K H I ~ ~ ~			
	351			
GNS1	K P Q H R R K R			
SUR4	~ ~ ~ ~ ~			
MAELO	~ ~ ~ ~ ~			

Figure 9

SCORES Initl: 153 Initn: 199 Opt: 495
57.4% identity in 549 bp overlap

MAELO	150	160	170	180	190	200
	TCTCGAACCAGAGAGAGGTGCGCATGTGGACTATCACTTACTTCGTGTCATCTTTGGTG					
S78624						
	5990	6000	6010	6020	6030	6040
MAELO	210	220	230	240	250	260
	GTGGCCAGATCATGAAGAAGCAG--GAAGGC-TTCAAGCTCAAGGCCCTCTTCATCCTCC					
S78624						
	6050	6060	6070	6080	6090	6100
MAELO	270	280	290	300	310	320
	ACAACTTCCTCCTGAGGATGCGCTCC--GGATGCTGTGTGCTCCTGTTTCATGAGAACT					
S78624						
	6110	6120	6130	6140	6150	6160
MAELO	330	340	350	360	370	380
	GGTCCCATCTCTGCGCAGAAAGGACTTTTCTAAGGATCTGCGAGCAGCGTGGCTGGAC					
S78624						
	6170	6180	6190	6200	6210	6220
MAELO	390	400	410	420	430	440
	CCAGCGCTCTGAGCTCTCTACTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG					
S78624						
	6230	6240	6250	6260	6270	6280
MAELO	450	460	470	480	490	500
	CAAGCTCTCTTTTGGTCTCAAGAGAGAGCTCTTGAATTCCTGCACTTCTCCACCTCTC					
S78624						
	6290	6300	6310	6320	6330	6340
MAELO	510	520	530	540	550	
	GATGACCATGCTTCTCTGCTTGT---CAAGCTTGGAGGATA-CACTTCAGTGTCTTGG					
S78624						
	6350	6360	6370	6380	6390	6400
MAELO	560	570	580	590	600	610
	GTGCTTATTACCTCAAGTGTGCTCAAGTCTTCAATGTAAGTCAAGTCAAGTCAAGTCAAG					
S78624						
	6410	6420	6430	6440	6450	
MAELO	620	630	640	650	660	670
	GTGCTC---GGTGTGCGCATCTGCTGGAGGAGTACTTGAACACTCTCCAGATCGTCCAG					
S78624						
	6460	6470	6480	6490	6500	6510
MAELO	680	690	700	710	720	730
	TTGGTCTTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG					
S78624						
	6520	6530	6540	6550	6560	6570

Figure 10A

Host(plasmid)	334pCGN7875)	334pYES2)	334pYX242)	334pRAE-5)	334pRAE-6)	334pYX242)	334pRAE-5)
Added substrate	25 μ M OA	25 μ M OA	25 μ M GLA	25 μ M GLA	25 μ M GLA	no substrate	no substrate
Fatty acid	lipid (μ g)	lipid (μ g)	lipid (μ g)	lipid (μ g)	lipid (μ g)	lipid (μ g)	lipid (μ g)
C16:0	11.948	23.601	35.123	92.011	85.160	16.294	25.34
C16:1	30.665	71.217	32.789	315.464	115.456	56.183	113.913
C18:0	6.185	9.704	10.515	22.628	18.879	5.535	11.092
C18:1n-9	35.340	57.429	33.989	154.386	106.881	28.388	51.538
C18:3n-6			48.856	58.084	12.434		
C20:0			0.474	0.710	0.244		
C20:1n-9	(0.375%)* 0.352	(0.309%)* 0.527		1.405	0.867		0.516
C20:3n-6	ND	ND	(0.092%)* 0.226	(0.324%)* 2.504	(0.269%)* 1.006	ND	ND
C22:0				0.460			
C22:1n-9				0.321	0.315		0.999
C24:0					1.825		
Total Lipid	93.760	170.490	245.090	771.690	374.420	112.99	256.52
ND = Not Detected							
% total fatty acid							

Figure 10B

Host(plasmid)	334(pYY242)	334(pYY242)	334(pRAE-5)	334(pRAE-5)	334(pRAE-6)
Added substrate	25 μ M GLA	25 μ M GLA	25 μ M GLA	25 μ M GLA	25 μ M GLA
Fatty acid	lipid (μ g)	lipid (μ g)	lipid (μ g)	lipid (μ g)	lipid (μ g)
C16:0	60.683	61.487	100.998	96.193	66.761
C16:1	79.838	79.586	359.754	220.440	87.359
C18:0	9.784	10.106	15.317	15.165	16.744
C18:1n-9	38.536	39.936	108.472	89.637	71.631
C18:3n-6	17.974	17.833	82.866	56.596	17.766
C20:0			0.510	0.570	
C20:1n-9					
C20:3n-6	(0.136%) * 0.389	(0.130%) * 0.374	(0.336%) * 3.035	(0.401%) * 2.689	(0.353%) * 1.185
C22:0			0.414		
C22:1n-9				0.383	
C24:0			1.513	1.626	
Total Lipid	285.560	288.045	902.560	671.113	335.496
*% total fatty acid					

Figure 12

Host(plasmid)	334(pYX242)	334(pRAE-5)	334(pRELO-1)	334(pRELO-2)
Added substrate	25 μ M GLA 25°C/48hrs	25 μ M GLA 25°C/48hrs	25 μ M GLA 25°C/48hrs	25 μ M GLA 25°C/48hrs
Fatty acid	Lipid (μ g)	Lipid (μ g)	Lipid (μ g)	Lipid (μ g)
C16:0	28.7	76.707	84.424	77.445
C16:1	0.729	2.513	1.532	1.056
C18:0	7.432	15.761	27.17	21.32
C18:1n-9	28.9	77.323	109.419	82.844
C18:3n-6	9.729	29.236	19.085	18.804
C20:0		0.643	0.522	0.537
C20:1n-9		0.77	0.426	0.299
C20:3n-6	(0.185%) * 0.374	(0.279%) * 1.472	(0.153%) * 0.748	(0.200%) * 0.832
C22:0		0.451		
C22:1n-9			0.224	
C24:0		0.918		
Total Lipid	202	527	490	416
*%total fatty acid				

Figure 11

Host(plasmid)	334(pRAE-5/pCCGR4)	334(pYXX242/pYES2)	Host(plasmid)	334(pRAE-5/pCCGR4)	334(pYXX242/pYES2)
Added substrate	25 μ M GLA	25 μ M GLA	Added substrate	25 μ M GLA	25 μ M GLA
Fatty Acid	lipid (μ g)	lipid (μ g)		lipid (μ g)	lipid (μ g)
C16:0	41.050	37.169	C16:0	96.986	32.221
C16:1	99.393	100.552	C16:1n-7	209.667	62.757
C18:0	34.432	27.852	C18:0	80.418	14.027
C18:1	110.631	92.786	C18:1n-9	207.104	28.701
C18:3n-6	15.004	7.924	C18:3n-6	25.264	10.543
C20:0	0.643	0.574	C20:0	2.038	
C20:1	1.996	1.684	C20:1n-9	3.591	
C20:3n-6	0.542	0.607	C20:3n-6	1.284	0.326
C20:4n-6	0.579		C20:4n-6	1.392	
C22:0	1.242	2.604	C22:0	1.124	
C24:0	4.754	4.563	C24:0	3.952	
Total Lipid	334	300	Total Lipid	756	197

Figure 13

SCORES Init1: 156 Initn: 215 Opt: 296
 Smith-Waterman score: 296; 28.8% identity in 264 aa overlap

	10	20	30	40	50	60
U61954	RTFKMMDQILGTNFTYEGAKEVARGLEGFSAKLAVGYIATIFGLKYYMKDRKAFDLSTPL					
MAELO	AQAYELVTGKSIDSFVFQEGVTPLSTQREVAMWTITYFVVIFGGRQIMKSQDAFKLK-PL					
	30	40	50	60	70	80
	70	80	90	100	110	119
U61954	NIWNGILSTFSLLGFLFTF-PTLLSVIRKDGFSHTYSHVSELYTDSTSGYWI-----F					
MAELO	FILHNFLLLTIASGSLLLLFIEENLVPILARNGL-----FYAICDDGAWTQRLLELLYY					
	90	100	110	120	130	
	130	140	150	160	170	
U61954	LWVISKIPELLDTVFIVLRKRPLIFMHWYHHALTGYVALVCYHE--DAVHVMVWV-VWMNY					
MAELO	LNYLVKYWELADTVFLVLKKKPLEFLHYFHHSMT---MVLCFVQLGGYTSVSWVPITLNL					
	140	150	160	170	180	190
	180	190	200	210	220	230
U61954	IIHAFMYGYLLKSLKVPIPPSVAQAITSQMVFQFA-----VAIFAQVHVSYKHYVEGVE					
MAELO	TVHVFMYYYYMRSAAGVRI--WWKQYLTTLQIVQFVLDLGFIFYFCAYTYFAFTYFPWAPN					
	200	210	220	230	240	250
	240	250	260	270	280	
U61954	-GLAYSFRGTAI-GFFMLTTYFYLWIFIQFYKEHYLKNKGKKYNLAKDQAKTQTKKAN					
MAELO	VGKCAGTEGAALFGCGLLSSYLLLFIFYRITY----NAKAKAAKERGSNFTPKTVKSGG					
	260	270	280	290	300	
MAELO	SPKKPSKSKHIX					
	310					

Figure 14

SCORES Init1: 178 Initn: 178 Opt: 318
 Smith-Waterman score: 318; 33.0% identity in 188 aa overlap

	50	60	70	80	90	100
Z68749	SLLTNQDEVFPHIRARRFIQEHFGLFVQMAIAYVILVFSIKRFMRDREPFQLTTALRLWN					
				: :: : :: : :: : :: :	:	
MAELO	ELVTGKSIDSFVFQEGVTPLSTQREVAMWTITYFVVIFGGRQIMKSQDAFKLKPLFILHN					
	30	40	50	60	70	80

	110	120	130	140	150	160
Z68749	FFLSVFSIYGSWTMFPF--MVQQIRLYGLYGCGCEALSNLPSQAEYWLFLTILSKAVEFV					
	: :	:: : : :	: :	: : :	: :	: :
MAELO	FLLTIAS--GSLLLLFIEHLVPILARNGLFYAICDD-GAWTQRLELLYLYNLVVKYWELA					
	90	100	110	120	130	140

	170	180	190	200	210	220
Z68749	DTFFLVLRKKPLIFLHWYHHMATFVFFCSNYPTPSSQSRVGVIVNLFVHAFMYPYFTRS					
	:	:	: :	: : :	:	: :
MAELO	DTVFLVLKKKPLEFLHYFHHSMTMVLCFVQLGGYTSVSWVPITLNLTVHVFMYYYMRS					
	150	160	170	180	190	200

	230	240	250	260	270
Z68749	MNIKVPAKISMAVTVLQLTQF--MCFIYGCTLMYYSLATNQARYPSNTPATLQCLSYTL				
	: : :	: : : :	: :	: : : :	
MAELO	AGVRIWWK--QYLTTLQIVQFVLDLGFYFCAITYFAFTYFPWAPNVGKCAGTEGAALFG				
	210	220	230	240	250

	280
Z68749	HLL

MAELO	CGLLSSYLLLFINFYRITYNAKAKAAKERGSNFTPKTVKSGGSPKKPSKSKHIX				
	270	280	290	300	310

Figure 15

SCORES Init1: 30 Initn: 30 Opt: 40
 Smith-Waterman score: 49; 22.1% identity in 86 aa overlap

		10	20	30	40	
AF003134		MLYSITRRCYTFFVTSLSHFYQLYVTECLENVIFNVLVNGQSINSRWKD				
		: : : : : : :: : : : : :: :				
MAELO		MAAAILDKNVNFQIDQPFQIKLDTYFAQA---YELVTGKSIDSFVFQEGVT--PLSTQREV				
		10	20	30	40	50

	50	60	70	80	90	100
AF003134	AEKTITSFPPHF-----PQTFQOPHILTLHFLFFVSVTLVTVFKKPKCEFPHSLA					
	: :: ::::: : : :					
MAELO	AMWTITYFVVIFGGRQIMKSQDAFKLKPLFILHNFLLTIASGSLLLLFIENLVPIARNG					
	60	70	80	90	100	110

Figure 16

Mouse

SCORES Initl: 161 Inaln: 191 Opt: 325
Smith-Waterman score: 325; 28.8% identity in 285 aa overlap

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      10      20      30      39      40
U97107      MLTSMNFSRGLKMD--LMQPYDFETFDLRFLEEYWVSSF-----LIVV
      :::: : | :: | :: | : : | : : : :
MAELO      MAAAILDKVNFGLQPFQIFLLDYFAQAYELVTGKSIDSEVFQEGVTPLSTQREVAMWTI
      10      20      30      40      50      60

      50      60      70      80      90      100
U97107      VYLLLIWVGITYMFTREFSFLQRPILILWSFFLAIFSIIGTLRMWKFMATVMFTVGLKQTV
      :::: | : :::: :::: : | :::: | : : : : : : : : : :
MAELO      TTFVVIFFGQIMFSQDAFTLPLFILHIFLLTAS--GSL-LLLFIEMLV-PILARNGL
      70      80      90      100      110

      110      120      130      140      150
U97107      CFAYITDDAVVRFWSFLFLSKVV---ELGDTAFIILKRPFIIVHWHHST--VLLFTS
      :: | | :: : : : : : : :::: :::: | : :::: | : : : : | : :
MAELO      FYAICDDGAWTQRLLELLYYLNYLVKFWELADTVFLVLKKKPLEFLHYFHHSMTMVLCPVQ
      120      130      140      150      160      170

      180      190      200      210      220      230
U97107      FGYKTHFVPSGGWF-MTMNFGVHSVMITYTMMKAAFLKHPNLLPMVITSIQILQMVLG---
      : : : | : : : : : : : : : : : : : : : : : : : : : :
MAELO      LGGYTSV---SWVFITINLTVHVEMITYYIMRSAAGVR--IWWKQYLTTLQIVQFVLDLGF
      180      190      200      210      220      230

      240      250      260      270      280      290
U97107      -----TIFGILNYIWPQFEG-CHTTEHEFFWSHMLYGYFIFLFAHFFHPAYLRPEKIVA
      | :: : | : | | : : : | :::: | : : : : | : : |
MAELO      TYPFAYTYFAITYFPWAPNVGHCAGTEGAALFGCGLLSSYLLLFINEYRITY-NAKAFAA
      240      250      260      270      280      290

      300      310
U97107      SKSQX
      :
MAELO      KERGSEFTPTVFSGGSPHPSFSKHIX
      300      310

```

Human

SCORES Initl: 147 Inaln: 147 Opt: 211
Smith-Waterman score: 111; 23.7% identity in 150 aa overlap

```

      110      120      130      140      150      160
MAELO      NLVPILARNGLFYATCDDGAWTQRLLELLYYLNYLVKFWELADTVFLVLKKKPLEFLHYFH
      : : : : : : : : : : : : : : : :
AC004050      SLIIVVDLTYILPLCLPGDTIFILFQKLIPLHWHY
      10      20      30

      170      180      190      200      210      220
MAELO      HSMTHVLCPVQLGGYTSVSWVFITINLTVHVEMITYYIMRSAAGVR-IWWKQYLTTLQIV
      | : : : : : : : : : : : : : : : : : : : : :
AC004050      HITVLLYSWYSYKTMVAGSGWEMTMNYGVHVMITYYALRAAGFVSRFFAMEITLSQIT
      40      50      60      70      80      90

      230      240      250      260      270      280
MAELO      QFVLDLGFIFYFAITYFPWAPNVGHCAGTEGAALFGCGLLSSYLLLFINEYRITY
      : : : : : : : : : : : : : : : :
AC004050      QILMG-----CVVNYLVFC---WMQH-DQCHSHFQNIWSSSLMYLSYLVLFCHFFFEAY
      100      110      120      130      140

```

Figure 17

SCORES Init1: 87 Initn: 218 Opt: 232
 Smith-Waterman score: 272; 29.7% identity in 232 aa overlap

	40	50	60	70	80	90
MAELO	SFVVFQEGVTPPLSTQREVAMWTITYFVVIFGGRQIMKSQDAFKLKPLFILHNFLLTIASGS					
				: :	: :	: :
I05465	PRYKSQRMVPPGQLHPYVCLFCYLLTHCMAGTKIHEEPAAVLLPSILQLYNLGLTLLS--					
	20	30	40	50	60	70
	100	110	120	130	140	150
MAELO	LLLLFIENLVPI LARNGLFYAICDDGAWTQRLLELLYYL--NYLVKYWELADTVFLVLKKK					
	:	:	:	:	:	:
I05465	-LYMFYELVTGVWEGKYNFFCQGTRSAGESDMKILRVLWWYYFSLIEFMDTFFFILRKN					
	80	90	100	110	120	
	160	170	180	190	200	210
MAELO	--PLEFLHYFHH-SMTMVLCFVQLGGYTSVSWVPITLNLTVHVFMYYYY-MRSAAGVR--					
	:		:	:	:	:
I05465	NHQITVLHVYHHATMLNIWWFVMNWVPCGHSYFGATLNSFIHVLMSYYGLSSIPSMRPY					
	130	140	150	160	170	180
	220	230	240	250	260	270
MAELO	IWWKQYLTTLQIVQFVLDLGFYFCAITYFAFTYFPWAPNVGKCAGTEGAALFGCGLLSS					
	:	:	:	:	:	:
I05465	LWWKKYITQGQLVQFVLTIIQTTCG-----VFWP-----CSFPLGWLFFQIGYMIS					
	190	200	210	220	230	
	280	290	300	310		
MAELO	YLLLFINFYRITYNAKAKAAKERGSNFTPKTVKSGGSPKKPSKSKHIX					
	:				:	:
I05465	LIALFTNFYIQTYNKKGASRRKEHLKGHQNGSVAAVNGHTNSFPSPLENSVKPRKQRKDXQ					
	240	250	260	270	280	290

Figure 18

1 MGTDQGKTFT WEELAAHNTK DDLALLAIRGR VYDVTKFLSR HPGGVDTLLL
51 GAGRDVTPVF EMYHAFGAAD AIMKKYYVGT LVSNELPIFP EPTVFHKTIK
101 TRVEGYFTDR NIDPKNRPEI WGRYALIFGS LIASYQAQLF VPFVVERTWL
151 QVVFAIIMGF ACAQVGINPI HDASHFSVTH NPTVWKILGA THDFFNGASY
201 LVWMYQHMLG HHPYTNIAGA DPDVSTSEPD VRRIKPNQKW FVNHNQHMF
251 VPFLYGLLAF KVRIQDINIL YFVKTNDAIR VNPISTWHTV MFWGGKAFFV
301 WYRLIVPLQY LPLGKVLLLF TVADMVSSYW LALTFQANHV VEEVQWPLPD
351 ENGIIQKDW A MQVETTQDY AHDShLWTSI TGSlnYQAVH HLFpNVSQHH
401 YPDILAIKN TCSEYKVPYL VKDTFWQAFA SHLEHLRVLG LRPKEE*

Figure 19

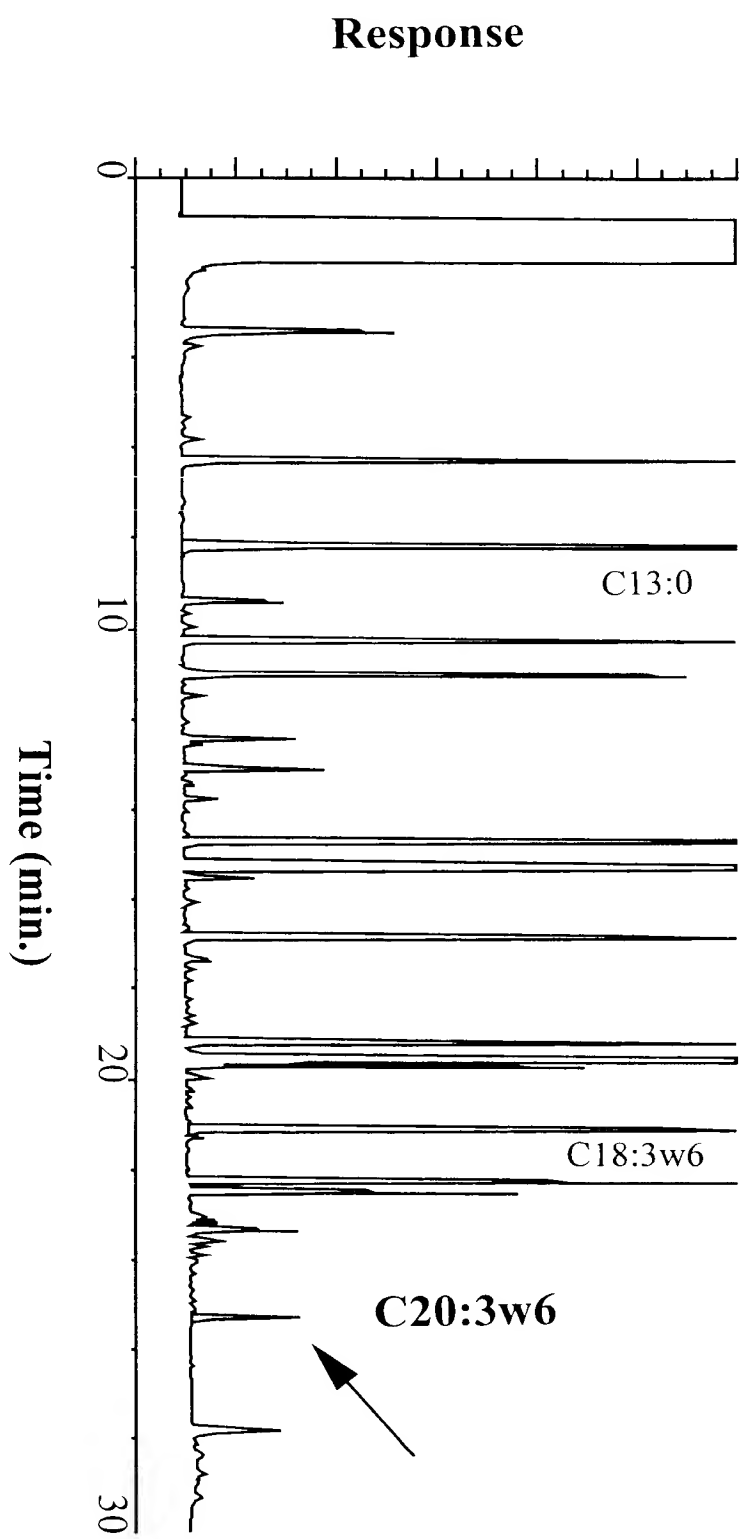


Figure 20

Host(plasmid)	334(MAD708-2)	334 (MAD708-10)	334(MAD708-18)	334 (MAD708-19)	334(MAD708-30)	334 (pRAE5)
Added substrate	25μM GLA	25μM GLA	25μM GLA	25μM GLA	25μM GLA	25μM GLA
Fatty Acid	% total lipid					
C16:0	14.1	14.68	14.38	15.45	14.13	13.59
C16:1	42.84	43.42	42.57	38.03	43.58	43.98
C18:0	3.19	3.28	3.63	4.08	3.37	2.04
C18:1n-9	17.66	19.39	19.6	20.8	20.06	10.88
C18:3n-6	6.65	5.58	10.24	9.46	3.56	11.14
C20:0	0.26	0.3	0.32	0.4	0.46	0.57
C20:3n-6	(47.5%) 6.03	(41.2%) 3.92	(8.0%) 0.91	(21.5%) 2.59	(49%) 3.43	(3.4%) 0.24
Total Lipid (μg)	238.47	307.86	188.51	167.31	207.47	466.65

(% conversion) = product/(substrate+product)

Figure 21

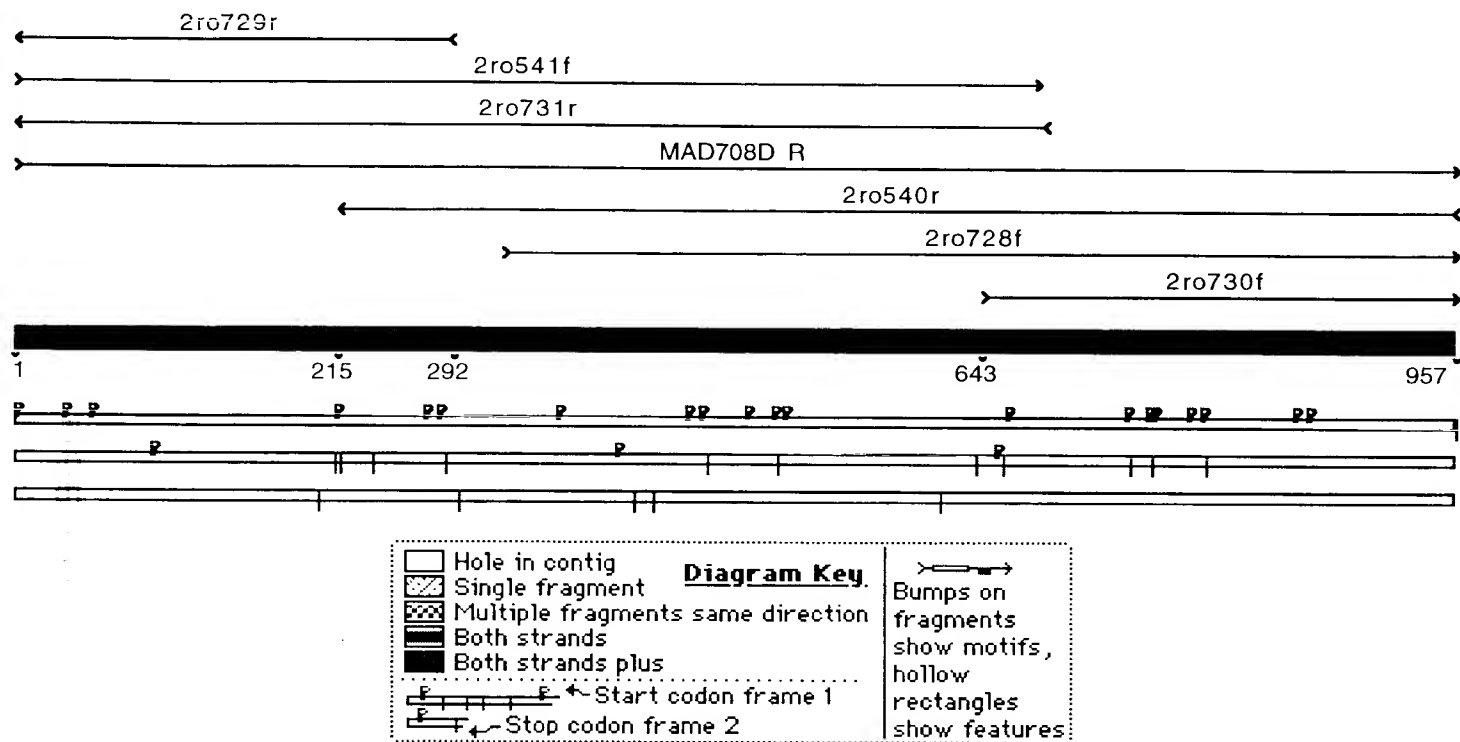


Figure 22

1	ATGGAGTCGA	TTGCGCCATT	CCTCCCATCA	AAGATGCCGC	AAGATCTGTT
51	TATGGACCTT	GCCACCGCTA	TCGGTGTCCG	GGCCGCGCCC	TATGTCGATC
101	CTCTCGAGGC	CGCGCTGGTG	GCCCAGGCCG	AGAAGTACAT	CCCCACGATT
151	GTCCATCACA	CGCGTGGGTT	CCTGGTCGCG	GTGGAGTCGC	CTTTGGCCCCG
201	TGAGCTGCCG	TTGATGAACC	CGTTCCACGT	GCTGTTGATC	GTGCTCGCTT
251	ATTTGGTCAC	GGTCTTTGTG	GGCATGCAGA	TCATGAAGAA	CTTTGAGCGG
301	TTCGAGGTCA	AGACGTTTTT	GCTCCTGCAC	AACTTTTGTC	TGGTCTCGAT
351	CAGCGCCTAC	ATGTGCGGTG	GGATCCTGTA	CGAGGCTTAT	CAGGCCAACT
401	ATGGACTGTT	TGAGAACGCT	GCTGATCATA	CCTTCAAGGG	TCTTCCTATG
451	GCCAAGATGA	TCTGGCTCTT	CTACTTCTCC	AAGATCATGG	AGTTTGTCTGA
501	CACCATGATC	ATGGTCCTCA	AGAAGAACAA	CCGCCAGATC	TCCTTCTTGC
551	ACGTTTACCA	CCACAGCTCC	ATCTTCACCA	TCTGGTGGTT	GGTCACCTTT
601	GTTGCACCCA	ACGGTGAAGC	CTACTTCTCT	GCTGCGTTGA	ACTCGTTCAT
651	CCATGTGATC	ATGTACGGCT	ACTACTTCTT	GTCGGCCTTG	GGCTTCAAGC
701	AGGTGTCGTT	CATCAAGTTC	TACATCACGC	GCTCGCAGAT	GACACAGTTC
751	TGCATGATGT	CGGTCCAGTC	TTCTTGGGAC	ATGTACGCCA	TGAAGGTCCT
801	TGGCCGCCCC	GGATACCCCT	TCTTCATCAC	GGCTCTGCTT	TGGTTCTACA
851	TGTGGACCAT	GCTCGGTCTC	TTCTACAAC	TTTACAGAAA	GAACGCCAAG
901	TTGGCCAAGC	AGGCCAAGGC	CGACGCTGCC	AAGGAGAAGG	CAAGGAAGTT
951	GCAGTAA				

Figure 23

1 MESIAPFLPS KMPQDLFMDL ATAIGVRAAP YVDPLEAALV AQAKEYIPTI
51 VHHTRGFLVA VESPLARELP LMNPFHVLLI VLAYLVTVFV GMQIMKNFER
101 FEVKTFSLH NFCLVSISAY MCGGILYEAY QANYGLFENA ADHTFKGLPM
151 AKMIWLFYFS KIMEFVDTMI MVLKKNNRQI SFLHVVHHSS IFTIWWLVTF
201 VAPNGEAYFS AALNSFIHVI MYGYYFLSAL GFKQVSFIKF YITRSQMTQF
251 CMMSVQSSWD MYAMKVLGRP GYPFFITALL WFYMWTMLGL FYNFYRKNK
301 LAKQAKADAA KEKARKLQ*

Figure 24

Host(plasmid)	334(pRPB2)	334 (pYES2)
Added substrate	25µM GLA	25µM GLA
	(n=4)	
Fatty Acid	% total lipid	
C16:0	15.65	15.23
C16:1	35.2	38.59
C18:0	5.68	5.55
C18:1n-9	25.55	25.27
C18:3n-6	3.1	6.75
C20:0	0.36	0.14
C20:3n-6	(62.0%) 5.06	(2.6%) 0.18
Total Lipid (µg)	314	247

(% conversion) = product/(substrate+product)

Figure 25

A.		334(pRPB2)	334(pRPB2)	334(pRPB2)	334(pRPB2)	334(pRPB2)	334(pRPB2)
Host(plasmid)	25μM SA	25μM OA	25μM LA	25μM DGLA	25μM AA	25μM Adenic	
Added substrate	C18:0	C18:1n-9	C18:2n-6	C20:3n-6	C20:4n-6	C22:4n-6	
Fatty Acid	% total lipid						
C16:0	15.07	14.52	15.74	15.69	16.06	15.15	
C16:1	33.7	32.37	32.23	25.65	33.65	33.39	
C18:0	*9.78	5.83	5.61	8.33	4.52	5.35	
C18:1n-9	31.2	*37.25	26.05	20.15	24.54	28.54	
C18:2n-6			*10.4				
C18:3n-6							
C20:2n-6			0.29				
C20:3n-6				*16.5			
C20:4n-6				0.27	*11.7		
C22:4n-6						*7.46	
Total Lipid (μg)	132	130	171	55	225	163	

B.		334(pRPB2)	334(pRPB2)	334(pRPB2)
Host(plasmid)	25μM ALA	25μM STA	25μM EPA	
Added substrate	C18:3n-3	C18:4n-3	C20:5n-3	
Fatty Acid	% total lipid			
C16:0	17.32	16.01	20.67	
C16:1	27.68	34.31	50.7	
C18:0	6.75	5.39	6.14	
C18:1n-9	28.4	28.54		
C18:3n-3	*8.39			
C18:4n-3		*1.95		
C20:4n-3		(73.2%) 5.33		
C20:5n-3			*10.33	
C22:5n-3			0.25	
Total Lipid (μg)	114	199	201	

*indicates substrate added
 (% conversion) = product/(substrate+product)

Figure 26

A.

Host(plasmid)	334(pRPB2+PRPE31)	334(pYES2+pYX242)
Added substrate	25μM GLA	25μM GLA
Fatty Acid	% total lipid	
C16:0	15.54	18.26
C16:1	30.16	33.51
C18:0	8.76	5.58
C18:1n-9	27	27.37
C18:3n-6	*2.6	*5.6
C20:0	0.4	0.32
C20:3n-6	(57.4%) 3.55	(2.9%) 0.17
C20:4n-6	(27.6%) 1.32	ND
Total Lipid (μg)	254	258

B.

Host(plasmid)	334(pRPB2+PRPE31)	334(pYES2+pYX242)
Added substrate	25μM STA	25μM STA
Fatty Acid	% total lipid	
C16:0	18	16.4
C16:1	28.37	34.78
C18:0	7.42	5.71
C18:1n-9	26.44	30.15
C18:4n-3	*2.93	*4.57
C20:0	0.25	0.17
C20:4n-3	4.13	0.32
C20:5n-3	(39%) 1.87	(2.1%) .10
Total Lipid (μg)	257	304

* indicates substrate added
(% conversion) = product/(substrate+product)

Figure 27

SCORES Initl: 114 Initn: 278 Opt: 278
 Smith-Waterman score: 308; 30.9% identity in 259 aa overlap

	40	50	60	70	80	90	99
GLELO	VAQAEKYIPTIVHHTRGFLVAVESPLARELPLMNPFHVLLIVLAYLVTVFVGMQIMKNFE						
	: : : :: : :: : :						
MAELO	GIKLDTYFAQAYELVTGKSIDSFVFQEGVTPSTQREVAMWTITYFVVIFGGRQIMKSQD						
	20	30	40	50	60	70	
	100	110	120	130	140	150	
GLELO	RFEVKTFSLHNFCLVSI SAYMCGGILYE--AYQANYGLFENAADHTFKGLPMAMKIWL						
	:: : : : : : : : : : : :						
MAELO	AFKLLKPLFILHNFLLTIASGSLLLFIENLVPILARNGLFYAICDDGAWTQRLLELLYYLN						
	80	90	100	110	120	130	
	160	170	180	190	200	210	
GLELO	YFSKIMEFVDTMIMVLKKNRQISFLHVVHSSIFTIWWLVTFVAPNGEAYFSAALNSFI						
	: : : : : : : : : : : : : : : : : :						
MAELO	YLVKYWELADTVFLVLKK--KPLEFLHYFHHS--MTMVLCFVQLGGYTSVSWVPITLNLTV						
	140	150	160	170	180	190	
	220	230	240	250		260	
GLELO	HVIMYGYFSLSALGFKQVSFIKFYITRSQMTQF-----CMMSVQS----SWDMYAM						
	: : : : : : : : : : : : : :						
MAELO	HVFMYYYMRSAAGVRI--WWKQYLTTLQIVQFVLDLGFYFCAYTYFAFTYFPWAPNVG						
	200	210	220	230	240	250	
	270	280	290	300	310		
GLELO	KVLGRPGYPFFITALLWFYMWTLGLFYNFYRKNALAKQAKADAAKEKARKLQ						
	: : : : : : : :						
MAELO	KCAGTEGAALFGCGLLSSYLL----LFINFYR----ITYNAKAKAAKERGSNFTPKTIVKS						
	260	270	280	290	300		
MAELO	GGSPKKPSKSKHIX						
	310						

Figure 28

GLELO	1	-MESIAPFLPSKMPQDLFMDLATAIGVRAAPYVDPLEAALVAQ	42
MAELO	1	-----MAAAILDKVNFIDQPFGLK	20
GNS1	1	-----MNSLVTQYAAPLFEERYPOLHXYLPTLERPFNISLW	36
SUR4	1	MNTTSTSTVIAAVADQFQSLNSSSCFLKVHVPSTIENP-FGIEL	42
GLELO	43	AEKYIPTIVHHTRGFLVAVESPLARELPLMNPFHVLLIVLAYL	85
MAELO	21	LDTYFAOAYELVTGKSIDSEFVFOEGVTPPLSTQREVAMWTITYF	63
GNS1	37	EHFDDDVVTRVTNGRFVPSSEFOFIAGELPLSTLPVLYAITAXY	79
SUR4	43	WPIFSKVFEYFSG-YPAEQFEFIHNKTFLANGYHAVSIIIVYX	84
GLELO	86	VTVFVGMQIMKNFERFEVKTFSLHNFCLVSIAYMCGGILYE	128
MAELO	64	VVIFGGROIMKSODA--FKLKLFIHNFLLTIASSGLLLFI	104
GNS1	80	VIIFFGGRLIS--KSKPFLNGLFQHLNLVLTSLTLLLMV	120
SUR4	85	IIIFGGQAILRALNASPLKFKLLFEIHNLFLLTSLISLVLLML	127
GLELO	129	--AYO--ANYGLFENAADHTFKGLPMAKMIMLFFYSKIMEFVD	167
MAELO	105	ENLVPILARNGLFYAICDDGAWTORLELLXYLNYLVKYMELAD	147
GNS1	121	EOLVPIIVQHGLFYAICNIGAWTORLVTLLXYMNYIVKFIEFID	163
SUR4	128	EOLVPMVYHNGLFWSCSKAEAFAPKLVTLXYLNYLTKFVELID	170
GLELO	168	TMIMVLKKNNRQISFLHVYHHSSTIFTIMWLVTFFVAPNGEAYFS	210
MAELO	148	TVFLVLKK--KPLEFLHYFHHSMTMVLCF-VOLGGYTSVSWVP	187
GNS1	164	TFFLVLKH--KKLTFLHTYHHGATALLCY-TOLMGTTSSISWVP	203
SUR4	171	TVFLVLR--KKLLFLHTYHHGATALLCY-TQLIGRTSVEWV	210
GLELO	211	AALNSFIHVIMYGYFFLSALGFKQVSFIKFYITRSOMTOFCMM	253
MAELO	188	ITLNLTVHVFMYYYYMRSAAAGVR--IWWKQYLTTLQIVOFVLD	228
GNS1	204	ISLNLGVHVVMYYFFLAARGIR--VWWKQWVTRFOIIOFVLD	244
SUR4	211	ILLNLGVHVIMYYFFLSSCGIR--VWWKQWVTRFOIIOFLID	251
GLELO	254	SVOSSWDMYAMKVLGRPGYPFFITALLWFYMWMTMLGLFYNFYR	296
MAELO	229	LGFIYFCAYTYFAFTYFPW-APNVGKCCAGTEGAALFGGLISS	270
GNS1	245	IGFIYFAVYOKAVHLYFP-ILPHCGDCVGSSTTATFAGCAIISS	286
SUR4	252	LVFVYFATYTFYAHKYLIDGILPNKGTCTCYGTQAAAAAYGYLILTS	294
GLELO	297	KNAKLAKOAKADAAREKARKLQ	318
MAELO	271	YLLLFINFYRITYNAKAKAAKERGSNFTPKTVKSGGSPKPKPSK	313
GNS1	287	YLLLFISFYINVYKRRGTTKTSRVVKRAHGGVAAKVNNEYVNVDL	329
SUR4	295	YLLLFISFYIQSYKKKGKKTVKKESEVSGSVASGSSSTGVKTSN	337
MAELO	314	SKHI	317
GNS1	330	KNVPTPSPSPKPOHRRKR	347
SUR4	338	TKVSSRKA	345

Figure 29

SCORES Init1: 83 Initn: 186 Opt: 271
 Smith-Waterman score: 297; 28.5% identity in 242 aa overlap

	30	40	50	60	70	80
MAELO	YELVTGKSIDSFVFQEGVTPLSQREVAMWTITYFVVIFGGRQIMKSQDAFKLKPLFILH					
					:	:
HS1	STYFKALLGPRDTRVKGWFLLDNYIPTFICSVIYLLIVWLGPKYMRNKQPFSCRGILVVY					
	10	20	30	40	50	60
	90	100	110	120	130	140
MAELO	NFLLTIASGSLLLLFIEENLVPILARNGLFYAICDDGAWTQRLELLYYL--NYLVKYWELA					
	:	:	:	:	:	:
HS1	NLGLTLLS---LYMFCELVTVGWEGKYNFFCQGTRTAGESDMKIIRVLWWYFYSKLIEFM					
	70	80	90	100	110	120
	150	160	170	180	190	200
MAELO	DTVFLVLKK--KPLEFLHYFHH-SMTMVLCFVQLGGYTSVSWVPITLNLTVHVFMYYYY-					
	:	:	:	:	:	:
HS1	DTFFFILRKNNHQITVLHVYHHASMLNIWWFVMNWVPCGHSYFGATLNSFIHVLMSYYG					
	130	140	150	160	170	180
	210	220	230	240	250	260
MAELO	MRSAAGVR--IWWKQYLTTLQIVQFVLDLGFYFCAITYFAFTYFPWAPNVGKCAGTEGA					
	:	:	:	:	:	:
HS1	LSSVPSMRPYLWKKYITQGQLLQFVLT-IQTSCGVI-----W-P-----CTFPLGW					
	190	200	210	220		230
	270	280	290	300	310	
MAELO	ALFGCGLLSSYLLLFINFYRITYNAKAKAAKERGSNFTPKTVKSGGSPKKPSKSKHI					
	:	:	:	:	:	:
HS1	LYFQIGYMISLIALFTNFYIQTYNKKGASRRKDHLKDHQNGSMAAVNGHTNSFSPLENNV					
	240	250	260	270	280	290
HS1	KPRKLRKDX					
	300					

Figure 30

SCORES Init1: 88 Initn: 208 Opt: 272
 Smith-Waterman score: 279; 28.2% identity in 266 aa overlap

	30	40	50	60	70	80
MAELO	QAYELVTGKSIDSFVFQEGVTPLSTQREVAMWTITYFVVIFGGRQIMKSQDAFKLKPLFI					
HS2	VNLYQEVMMKHADPRIQGYPLMGSPILLMTSILLTYVYFVLSLGPR-IMANRKPFQLRGFMI					
	10	20	30	40	50	60
	90	100	110	120	130	140
MAELO	LHNFLLTIASGSLLLJFTEN--LVPILAR-NGLFYAICDDGAWTQRLLELLYYLNYLVKYW					
HS2	VYNFSLVALSLYIVYEFLMSGWLSTYTWRCDPVDYSNSPEALRMVRVAWLFLFS---KFI					
	70	80	90	100	110	120
	150	160	170	180	190	
MAELO	ELADTVFLVLKFK--PLEFLHYFHHSMT---MVLCFVQLGGYTSVSWVPITLNLTVHVF					
HS2	ELMDTVIFILRKKGQVTFHVFHHSVLPWSWWWGVKIAPGGMGSFHAM---INSSVHVI					
	130	140	150	160	170	
	200	210	220	230	240	
MAELO	MYYYMRSAGV---RIWWKQYLTTLQIVQFVL---DLGFIYF---CAYTYFAFTYFPW					
HS2	MYLYYGLSAFGPVAQPYLWWKKHMTAIQLIQFVLVSLHISQYYFMSSCNYPVILHLIW					
	180	190	200	210	220	230
	250	260	270	280	290	300
MAELO	APNVGKCGATEGAALFGCGLLSSYLLLFIFYRITYNAKAKAAKERGSNFTPKTVKSGGS					
HS2	-----MYG---TIFFMLFSNFWYHSYTKGKRLPRALQONGAPGIAKVKAN					
		240	250	260	270	
	310					
MAELO	PKKPSKSKHI					
HS2	X					
	280					

Figure 31

SCORES Init1: 88 Initn: 207 Opt: 223
 Smith-Waterman score: 236; 30.4% identity in 191 aa overlap

	100	110	120	130	140	150
MAELO	LLLLFIENLVPIARNGLFYAICDDGAWTQRLLELLYYLNVLVKYWELADTVFLVLKKKP-					
	: : : : ::: :					
MM2	IVYEFLMSGWLSTYTWRCDPIDFSNSPEALRMVRVAWLFLSKVIELMDTVIFILRKKDG					
	20	30	40	50	60	70
	160	170	180	190	200	209
MAELO	-LEFLHYFHHSMTIMVLCF---VQLGGYTSVSWVPITLNLTVHVFMYYYMRSAGV---					
	: : : : : : :					
MM2	QVTFLHVFHHSVLPWSWWWGIKIAPGGMGSFHAM---INSSVHVVMYLYYGLSALGPVAQ					
	80	90	100	110	120	130
	210	220	230	240	250	260
MAELO	-RIWWKQYLTTLQIVQFVL---DLGFIYF---CAYTYFAFTYFPWAPNVGKCAGTEGAAL					
	: ::: : : : : : : : :					
MM2	PYLWWFKHMTAIQLIQFVLVSLHISQYYFMPSCNYQYPVIIHLIW-----M					
	140	150	160	170		
	270	280	290	300	310	
MAELO	FGCGLLSSYLLLLFINFYRITYNAKAKAAKERGSNFTPKTVKSGGSPKKPSKSKI					
	: : : : : : : : : : : :					
MM2	YG---TIFFILFSNFWYHSYTKGKRLPRAVQQNGAPATTKVKAN					
	180	190	200	210		

Figure 32

SCORES Init1: 51 Initn: 115 Opt: 168
 Smith-Waterman score: 168; 30.4% identity in 115 aa overlap

	30	40	50	60	70	80
MAELO	YELVTGKSIDSFVFQEGVTPLSTQREVAMWTITYFVWIFGGRQIMKSQDAFKLKPLFILH					
AI225632	NAFLDNMFGRDSRVRGWFLLDSTLPTFILTITYLLSIWLGKYMKNRPALSLRGILTLY					
	20	30	40	50	60	70
	90	100	110	120	130	140
MAELO	NFLLTIASGSLLLFIENLVPILARNGLFYAICDD---GAWTQRLELLYYLNYLVKYWE					
AI225632	NLAITLLSAYMLVELI-----LSSWEGGYNLQCQNLDSEGEVDVRVAKVLVWYYFSLKVE					
	80	90	100	110	120	
	150	160	170	180	190	200
MAELO	LADTVFLVLKFK--PLEFLHYFHHSMTMVLCFVQLGGYTSVSWVPITLNLTVHVFMYYYY					
AI225632	FLDTIFFVLRRKANQITFLHVYHHASMFNI					
	130	140	150			

Figure 33

SCORES Frame: (3) Init1: 332 Initn: 332 Opt: 384
40.3% identity in 144 aa overlap

	80	90	100	110	120	130
GLELO	LIVLAYLVTVFVGMQIMKNFERFEVKTFSLLHNFCLVSI SAYMCGGILYEAYQANYGL-F					
				: : :: : : :: :::: :		
AI815960	LYNLGITLLSAYMLAELILSTWEGGYNLQC					
				10	20	30
	140	150	160	170	180	190
GLELO	ENADHTFKGLPMAKMIWLFYFSKIMEFVDTMIMVLKKNRQISFLHVVYHHSSIFTIWWL					
	:: ::	: : ::	:	: : :: : : : : :	: : : : : : : : :	: : :
AI815960	QDLTSAGEADIRVAKVLWYYFYSKSVEFLDTIFFVLRKKTSQITFLHVVYHHASMFNIWWC					
	40	50	60	70	80	90
	200	210	220	230	240	250
GLELO	VTFVAPNGEAYFSAALNSFIHVIMYGYFLSAL-GFKQVSFIKFYITRSQMTQFCMMSVQ					
		::: : : : : : : : : :	: : : : : : : :	: : : : : : : :	: : : : : :	
AI815960	VLNWIPCGQSFFGPTLNSFIHILMYSYYGLSVFSPMHKYLWWKKYLTQAQLVQF					
	100	110	120	130	140	
	260	270	280	290	300	310
GLELO	SSWDMYAMKVLGRPGYPFFITALLWFYMWMTMLGLFYNFYRKNALAKQAKADAAKEKARK					

Figure 34

SCORES Initl: 316 Initn: 384 Opt: 477
 Smith-Waterman score: 477; 34.2% identity in 240 aa overlap

	50	60	70	80	90	100
GLELO	AQAKEYIPTIVHHTRGFLVAVESPLARELPLMNPFFHVLLIVLAYLVTVFVGMQIMKNFER					
HS1	MEHFDASLSTYFKALLGPRDTRVKGWFI.LDNYIPTFICSVIYLLIVWLGPKYMRNKQP					
	10	20	30	40	50	
	110	120	130	140	150	159
GLELO	FEVKTFSLLLHNFCVLSISAYMCGGILYEAYQANYGLF-ENAAADHTFKGLPMAKMIWLFYF					
HS1	FSCRGILVVYNLGLTLLSLYMFCELVGTGVWEGKYNFFCQGTRTAGESDMKIIIRVLWWYYF					
	60	70	80	90	100	110
	160	170	180	190	200	210
GLELO	SKIMEFVDTMIMVLKKNRQISFLHVVYHHSSIFTIWWLVTFVAPNGEAYFSAALNSFIHV					
HS1	SKLIEFMDTFFFILRKNNHQITVLHVVYHHASMLNIWWFVMNVWPCGHSYFGATLNSFIHV					
	120	130	140	150	160	170
	220	230	240	250	260	270
GLELO	IMYGYFLSAL-GFKQVSFIKFYITRSQMTQFCMMSVQSSWDMYAMKVLGRPGYPFFITA					
HS1	LMYSYGLSSVPSMRPYLWWKKYITQGQLLQFVLTIIQTS-----CGVIWPCTFPLGWLY					
	180	190	200	210	220	230
	280	290	300	310		
GLELO	LLWFYMWMTMLGLFYNFYRK--NAKLAKQAKADAAKEKARKLQ					
HS1	FQIGYIMISLIALFTNFYIQTYNKKGASRRKDHLKDHQNGSMAAVNGHTNSFSPLENNVKP					
	240	250	260	270	280	290

Figure 35

SCORES Init1: 80 Initn: 114 Opt: 178
 Smith-Waterman score: 178; 28.8% identity in 146 aa overlap

	140	150	160	170	180	190
GLELO	FENAADHTFKGLPMAKMIWLFYFSKIMEFVDTMIMVLKKNRQISFLHVYHHSSIFTIWW					
				::: :	::	
AC004050	DTIFIILRK--QKLIFLHWYHHITVLLYSW					
				10	20	
	200	210	220	230	240	250
GLELO	LVTfVAPNGEAYFSAALNSFIHVIMYGYFSLALGFKQVSFIKFYITRSQMTQFCMMSVQ					
	::	::	: :: :		:	:::
AC004050	YSYKDMVAGGGWF-MTMNYGVHAVMYSYYALRAAGFRVSRKFAMFITLSQITQMLMGCVV					
	30	40	50	60	70	80
	260	270	280	290	300	310
GLELO	SSWDMYAMKVLGRPGYPFFITALLW--FYMWTMLGLFYNFYRKN--AKLAKQAKADAAKE					
	: :	:	:		::	::: ::
AC004050	NYLVFCWMQ--HDQCHSHF-QNIFWSSLMYLSYLVLFCHFFFEAYIGKMRKTTKAEX					
	90	100	110	120	130	140
GLELO	KARKLQ					

Figure 36

SCORES Init1: 288 Initn: 288 Opt: 399
Smith-Waterman score: 399; 34.6% identity in 211 aa overlap

[illegible]

Figure 37

SCORES Init1: 160 Initn: 227 Opt: 269
 Smith-Waterman score: 269; 35.3% identity in 119 aa overlap

	50	60	70	80	90	100
GLELO	PTIVHHTRGFLVAVESPLARELPLMNPFHVLLIVLAYLTVFVGMQIMKNFERFEVKTFS					
	: : : : : : : : : : : : : :					
AI225632	NEVNAFLDNMFGPRDSRVRGWFLDSYLPFTILTITYLLSIWLGNKYMKNRPALSLRGIL					
	10	20	30	40	50	60
	110	120	130	140	150	160
GLELO	LLHNFCLVSISAYMCGGILYEAYQANYGLFENAADHTFKG-LPMAK-MIWLIFYFSKIMEF					
	: : : : : : : : : : : : : : : : : : : : :					
AI225632	TLYNLAITLLSAYMLVELILSSWEGGYNLQCQNLD SAGEGDVRVAKVLVW-YYFSKLVEF					
	70	80	90	100	110	120
	170	180	190	200	210	220
GLELO	VDTMIMVLKKNNRQISFLHVVHSSIFTIWWLVTFVAPNCEAYFSAALNSFIHVIMYGY					
	: : : : : : : : : : :					
AI225632	LDTIFFVLRKKANQITFLHVVHHA S M F N I					
	130	140	150			

Figure 38

SCORES Init1: 64 Initn: 129 Opt: 233
 Smith-Waterman score: 239; 23.7% identity in 279 aa overlap

	20	30	40	50	60	70
GLELO	FMDLATAIGVRAAPYVDPLEAALVAQAEKYIPTIVHHTRGFLVAVESPLAREL-----PL					
U97107	: :: : : : : : MDTSMNFSRGLKMDLMQPYDFETFQDLRPF 10 20 30					
	80	90	100	110	120	129
GLELO	MNPFHV--LLIVLAYLVTVFVGMQIMKNFERFEVKTFSLHNFCLVSI SAYMCGGILYEA					
U97107	:: : : :: : : : :: : :: : : : : : : : LEEYWSSFLIVVVYLLLVVVGQTYMRTRKSFSLQRPLILWSFFLAIFS--ILGTLRMWK 40 50 60 70 80					
	130	140	150	160	170	180
GLELO	YQAN---YGLFENAADHTFKGLPMAKMIW--LFYFSKIMEFVDTMIMVLKKNNRQISFL					
U97107	:: : : :: : : : : : :: : : :: : : : FMATVMFTVGLKQTVCFAIYTDDAVVRF-WSFLFLLSKVVELGDTAFIILRK--RPLIFV 90 100 110 120 130 140					
	190	200	210	220	230	240
GLELO	HVIYHSSI--FTIWVLVTFVAPNGEAYFSAALNSFIHVIMYGYFFLSALGFKQVSFIKFY					
U97107	:: : : : :: : : : : : : :: : HWYHHSTVLLFTSFGYKNKV-PSGGWFMT--MNFGVHSVMTYYTMKAARKHPNLLPMV 150 160 170 180 190 200					
	250	260	270	280	290	
GLELO	ITRSQMTQFCMMSVQSSWDMYAMKVLG--RPGYPFFITALLWFYMWMTMLGLFYN--FYRK					
U97107	: : : : : : : : : : : : : : : : ITSLQILQMVLGTIFGILNYIWRQEKGCHTTTEHFFWSFMLYGTIFYFILFAHFFHRAYLRP 210 220 230 240 250 260					
	300	310				
GLELO	NAKLAKQAKADAAKEKARKLQ					
U97107	: : : : : : KGKVASKSQ 270					

Figure 39

SCORES Init1: 100 Initn: 205 Opt: 271
Smith-Waterman score: 271; 30.7% identity in 218 aa overlap

	60	70	80	90	100	110
GLELO	TRGFLVAVESPLARELPLMNPFFHVLIVLAYLVTVFVGMQIMKNFERFEVKTFSLLHNFC					
				: :	: :	: :
U68749	ATHGPKNFPDAEGRKFFADHFDVTIQASILYMVVVFGTKWFMNRQPPQLTIPLNIWNFI					
(F56H11.4)	30	40	50	60	70	80

	120	130	140	150	160
GLELO	LVSISAYMCGGILYEAYQ--ANYGL---FENAADHTFKGLPMAKMIWLFYFSKIMEFVD				
	::	:	:	:	:::
U68749	LAAFSIAGAVKMTPEFFGTIANKGIVASYCKVDFDT-KG-ENGYVWVWLFMASKLFELVD				
(F56H11.4)	90	100	110	120	130

	170	180	190	200	210	220
GLELO	MIMVLKKNRQISFLHVYHHSSIFTIWWLVTFVAPNGEAYFSAALNSFIHVIMYGYFLS					
	::: :	:			:	:
U68749	IFLVLRK--RPLMFLHWYHHILTMIYAWYSHPLTP-GFNRYGIYLNFFVHAFMYSYYFLR					
(F56H11.4)	150	160	170	180	190	

	230	240	250	260	270	280
GLELO	ALGFKQVSFIKFYITRSQMTQFCMMSVQSSWDMYAMKVLGRP-GYPFFITALLWFYMW					
	:::	:		:	:	::
U68749	SMKIRVPGFIAQAITSQIVQFIISCAVLAHLGYLMHFTNANCDFEPSVFKLAVFMDTTY					
(F56H11.4)	200	210	220	230	240	250

	290	300	310
GLELO	LGLFYNFYRFNAKLAKQAKADAAKEKARKLQ		
	:	:	
U68749	LALFVNFFLQSYVLRGGKDKYKAVPKKKNN		
(F56H11.4)	260	270	280

Figure 40

SCORES Init1: 189 Initn: 264 Opt: 358
 Smith-Waterman score: 358; 28.7% identity in 296 aa overlap

	10	20	30	40	50	59
MAELO	MAAAILDKVNFGIDQPFQGIKLDTYFAQAYELVTGKSIDSFVFQEGVTPPLSTQREVAMW-T					
	::: : : : : : : : : : : : : : : :					
U68749	MAQHPLVQRLLDVKFDT---KRFVAIATHGPKNFPDAEGRKFFADHFDVTIQAS					
(F56H11.4)	10	20	30	40	50	

	60	70	80	90	100	110
MAELO	ITYFVVIFGGRQIMKSQDAFKLK-PLFILHNFLLTIASGSLLLLFIEENLVPILARNGLFY					
	: : : : : : : : : : : : : : : : :					
U68749	ILYMVVVVFGTKWFMNRNQPFQLTIPLNIW-NFILAASFAGAVKMTPEFFGTIANKGIVA					
(F56H11.4)	60	70	80	90	100	110

	120	130	140	150	160	170
MAELO	AICDDGAWTQRLELLYYLNYLV-KYWELADTVFLVLKKKPLEFLHYFHHSMTMVLCFVQL					
	: : : : : : : : : : : : : : : : : : : :					
U68749	SYCKVFDFTKGENGYVWVLFMASKLFELVDITFLVLRKRPLMFLHWYHHILTMIAWYSH					
(F56H11.4)	120	130	140	150	160	170

	180	190	200	210	220	230
MAELO	GGYTSVSWVPITLNLTVHVFMY-YYMRSAAAGVRI--WWKQYLTTLQIVQFVLDLGFYIF					
	: : : : : : : : : : : : : : : :					
U68749	PLTPGFNRYGIYLNFFVHAFMYSYYFLRSMK-IRVPGFIAQAITSQIVQFIISCAVLAH					
(F56H11.4)	180	190	200	210	220	

	240	250	260	270	280	
MAELO	CAYT-YFAFTYFPWAPNVGKAGTEGAALFGCGLLSSYLLLFINFYRITY-----NAKAK					
	: : : : : : : : : : : : : :					
U68749	LGYLMHFTNANCDFEPSVFKLA-----VF---MDTTYLALFVNFFLQSYVLRGGKDKYK					
(F56H11.4)	230	240	250	260	270	280

	290	300	310
MAELO	AAKERGSNFTPKTVKSGGSPKKPSKSKI		
	: : :		
U68749	AVPKKKNN		
(F56H11.4)			

Figure 41

SCORES Initl: 77 Initn: 155 Opt: 264
 Smith-Waterman score: 264; 27.2% identity in 206 aa overlap

	40	50	60	70	80	90
GLELO	AALVAQAKEYIPTIVHHTRGFLVAVESPLARELPLMNPFHVLLIVLAYLVTVFVGMQIMK					
				: :	::: ::: :	
DM1	PTKMINMDISVTPNYSYIFDFENDFIHQTRKWMLENWTWVFYYCGIYMLVIFGGQHFMQ					
	10	20	30	40	50	60

	100	110	120	130	140	150
GLELO	NFERFEVKTFSLHNFCLVSIAYMCGGILYEAYQA--NYGLFENAADHTF--KGLPMAK					
	::: :: : : : : :: : ::: :: : :					
DM1	NRPRFQLRGPLIIWNTLLAMFSIMGAARTAPELIHVLRYGLFHSVCVPSYIEQDRVCGF					
	70	80	90	100	110	120

	160	170	180	190	200	210
GLELO	MIWLFYFSKIMEFVDTMIMVLKKNNRQISFLHVYHHSSIFTIWWLVTFVAPNGEAYFSAA					
	: : : :: : : : :: : :: : : : :					
DM1	WTWLFVLSKLPGLGDTIFIVLRK--QPLIFLHWYHHITVLIYSWF-SYTEYTSSARWFIV					
	130	140	150	160	170	180

	220	230	240	250	260	270
GLELO	LNSFIHVIMYGYFLSALGFKQVSFIKFYITRSQMTQFCMMSVQSSWDMYAMKVLGRPGY					
	: : : : : : :: :: : : : : : :					
DM1	MNYCVHSVMSYYSYALKAAARFNPPRFISMIITSLQLAQMIIGCAINWANGFLKTHGTXS					
	190	200	210	220	230	240

	280	290	300	310
GLELO	PFFITALLWFYMWMTMLGLFYNFYRKNKAKLAKQAKADAAKEKARKLQ			
DM1	HISQRNINLSIAMYSSYFVLFARFFYKAYLAPGGHKSRMA			
	250	260	270	280

Figure 42

SCORES Init1: 181 Initn: 279 Opt: 328
Smith-Waterman score: 328; 30.0% identity in 237 aa overlap

	40	50	60	70	80	90
MAELO	VTGKSIDSFVFQEGVTP	LSTQREVAMW	TITYFVVI	FGGRQIMKSQDA	FKLKPLFILHNFL	
				::	::: ::	: : : :
DM1	IFDFENDFIHQ	RTRKWML	ENWNTWV	FYYCGIYMLV	IFGGQHFMQNR	PRFQLRGPLIIWNTL
	30	40	50	60	70	80
	100	110	120	130	140	149
MAELO	LTIASGSL	LLLFIE	NLVPIL	ARNGLFYA	ICDDGAWTQ	-RLELLY-YNLVKYWELADTV
	::	: : :	: ::	: :	::: :	: :
DM1	LAMFSIMGA	ARTAPE	LIHVL	RHYGLFHS	VCVPSYIEQ	DRVCGFWTWLFVLSKLP
	90	100	110	120	130	140
	150	160	170	180	190	200
MAELO	FLVLK	KKPLEF	LHYFHHS	MTMVL	CFVQLGGYTS	-VSWVPITLNLTVHVFMYYYYMRSAAG
	:	: :	::	::: : :	:	:: :
DM1	FIVLRKQ	PLIFL	HWYHHIT	VLIYSW	FSYTEYTSS	ARWF-IVMNYCVHSMYSYALKAAR
	150	160	170	180	190	200
	210	220	230	240	250	260
MAELO	VRI--	WWKQYL	TTLQIV	QFVLDL	GFIYFCA	YTYFAFTYFPWAPNVGKCAGTEGAALFGCG
	: : :	: :	::: :::	: :	:: : : :	:: : : :
DM1	FNPPRF	FISMIIT	SLQLA	QMIIG----	CAINW	ANGFLK-THGTXSCHISQRNINLSIA
	210	220	230	240	250	
	270	280	290	300	310	
MAELO	LLSSY	LLLLF	INFYR	ITYNA	KAKA	KERGSNFTPKTVKSGGSPKKPSKSKHI
	: :	:	:	: :	:	:
DM1	MYSSY	FVLFAR	FFYKAY	LAPGG	HKSRRMA	
	260	270	280			

Figure 43

1	ATGGAACATT	TTGATGCATC	ACTTAGTACC	TATTTCAAGG	CATTGCTAGG
51	CCCTCGAGAT	ACTAGAGTAA	AAGGATGGTT	TCTTCTGGAC	AATTATATAC
101	CCACATTTAT	CTGCTCTGTC	ATATATTTAC	TAATTGTATG	GCTGGGACCA
151	AAATACATGA	GGAATAAACA	GCCATTCTCT	TGCCGGGGGA	TTTTAGTGGT
201	GTATAACCTT	GGACTCACAC	TGCTGTCTCT	GTATATGTTC	TGTGAGTTAG
251	TAACAGGAGT	ATGGGAAGGC	AAATACAAC	TCTTCTGTCA	GGGCACACGC
301	ACCGCAGGAG	AATCAGATAT	GAAGATTATC	CGTGTCTCT	GGTGGTACTA
351	CTTCTCCAAA	CTCATAGAAT	TATGGACAC	TTTCTTCTTC	ATCCTGCGCA
401	AGAACAACCA	CCAGATCACG	GTCCTGCACG	TCTACCACCA	TGCCTCGATG
451	CTGAACATCT	GGTGGTTTGT	GATGAACTGG	GTCCCCCTGCG	GCCACTCTTA
501	TTTTGGTGCC	ACACTTAATA	GCTTCATCCA	CGTCCTCATG	TACTCTTACT
551	ATGGTTTGTC	GTCAGTCCCT	TCCATGCGTC	CATACCTCTG	GTGGAAGAAG
601	TACATCACTC	AGGGGCAGCT	GCTTCAGTTT	GTGCTGACAA	TCATCCAGAC
651	CAGCTGCGGG	GTCATCTGGC	CGTGCACATT	CCCTCTTGGT	TGGTTGTATT
701	TCCAGATTGG	ATACATGATT	TCCCTGATTG	CTCTCTTCAC	AACTTCTAC
751	ATTCAGACCT	ACAACAAGAA	AGGGGCCTCC	CGAAGGAAAG	ACCACCTGAA
801	GGACCACCAG	AATGGGTCCA	TGGCTGCTGT	GAATGGACAC	ACCAACAGCT
851	TTTCACCCCT	GGAAAACAAT	GTGAAGCCAA	GGAAGCTGCG	GAAGGATTGA
901	AGTCAAAGAA	TTGA			

Figure 44

1 MEHFDASLST YFKALLGPRD TRVKGWFLLD NYIPTFICSV IYLLIVWLGP
51 KYMRNKQPFS CRGILVVYNL GLTLLSLYMF CELVTGVWEG KYNFFCQGTR
101 TAGESDMKII RVLWYYYFSK LIEFMDTFFF ILRKNNHQIT VLHVYHHASM
151 LNIWWFVMNW VPCGHSYFGA TLNSFIHVLM YSYYGLSSVP SMRPYLWWKK
201 YITQGQLLQF VLTIIQTSCG VIWPCTFPLG WLYFQIGYMI SLIALFTNFY
251 IQTYNKKGAS RRKDHLKDHQ NGSMAAVNGH TNSFSPLENN VKPRKLRKD*

Figure 45

Host (plasmid)	334(pYX242)	334(pRAE-58-A1)	334(pYX242)	334(pRAE-58-A1)
Added substrate	25 μ M GLA	25 μ M GLA	25 μ M AA	25 μ M AA
Fatty acid	ϵ^7 total fatty acid	ϵ^7 total fatty acid	ϵ^7 total fatty acid	ϵ^7 total fatty acid
C18:3n-6	4.40	2.71	0.03	0.04
C20:3n-6	0.09	(50.34%)* 2.75	0.02	0.02
C20:4n-6			7.84	3.97
C22:4n-6			ND	(23.37%)* 1.21
C16:1n-7	41.11	34.72	41.49	35.07
C18:1n-7	1.85	11.33	2.01	11.57
C20:1n-7	0.04	1.48	0.04	1.62
C18:1n-9	15.60	15.66	15.16	14.57
C20:1n-9	0.06	0.22	0.06	0.23
C18:1n-5	0.11	0.62	0.12	0.58
Total Lipid	370	969	359	514

*% conversion=product/(substrate+product)

Figure 46

```
1  ATGGCTCAGC ATCCGCTCGT TCAACGGCTT CTCGATGTCA AATTCGACAC
51  GAAACGATTT GTGGCTATTG CTACTCATGG GCCAAAGAAT TTCCCTGACG
101 CAGAAGGTCG CAAGTTCTTT GCTGATCACT TTGATGTTAC TATTCAGGCT
151 TCAATCCTGT ACATGGTCGT TGTGTTTCGGA AAAAAATGGT TCATGCGTAA
201 TCGTCAACCA TTCCAATTGA CTATTCCACT CAACATCTGG AATTTCATCC
251 TCGCCGCATT TTCCATCGCA GGAGCTGTCA AAATGACCCC AGAGTTCTTT
301 GGAACCATTG CCAACAAAGG AATTGTCGCA TCCTACTGCA AAGTGTTTGA
351 TTTCACGAAA GGAGAGAATG GATACTGGGT GTGGCTCTTC ATGGCTTCCA
401 AACTTTTCGA ACTTGTTGAC ACCATCTTCT TGGTTCTCCG TAAACGTCCA
451 CTCATGTTCC TTCCTGGTA TCACCATATT CTCACCATGA TCTACGCCTG
501 GTACTCTCAT CCATTGACCC CAGGATTCAA CAGATACGGA ATTTATCTTA
551 ACTTTGTCGT CCACGCCTTC ATGTACTCTT ACTACTTCCT TCGCTCGATG
601 AAGATTCGCG TGCCAGGATT CATCGCCCAA GCTATCACAT CTCTTCAAAT
651 CGTTCAATTG ATCATCTCTT GCGCCGTTCT TGCTCATCTT GGTATCTCA
701 TGCACTTCAC CAATGCCAAC TGTGATTTTC AGCCATCAGT ATTCAAGCTC
751 GCAGTTTTCA TGGACACAAC ATACTTGGCT CTTTTCGTCA ACTTCTTCCT
801 CCAATCATAT GTTCTCCGCG GAGGAAAAGA CAAGTACAAG GCAGTGCCAA
851 AGAAGAAGAA CAACTAA
```

Figure 47

1 MAQHPLVQRL LDVKFDTKRF VAIATHGPKN FPDAEGRKFF ADHFDVTIQA
51 SILYMVVVFG TKWFMRNRQP FQLTIPLNIW NFILAAFSIA GAVKMTPEFF
101 GTIANKGIVA SYCKVFDFTK GENGYWVWLF MASKLFELVD TIFLVLRKRP
151 LMFLHWYHHI LTMIYAWYSH PLTPGFNRYG IYLNFVVHAF MYSYYFLRSM
201 KIRVPGFIAQ AITSLQIVQF IISCAVLAHL GYLMHFTNAN CDFEPSVFKL
251 AVFMDTTYLA LFVNFFLQSY VLRGGKDKYK AVPKKKNN

Figure 48

Host (plasmid)	334(pYX242)	334(pRET-21)	334(pRET-22)
Added Substrates	50 μ M GLA + 50 μ M AA	50 μ M GLA + 50 μ M AA	50 μ M GLA + 50 μ M AA
Fatty Acid	%total fatty acid	%total fatty acid	%total fatty acid
C16:0	9.22	12.46	9.9
C16:1	0.09	0.18	0.13
C18:0	1.46	2.41	1.49
C18:1n-9	4.03	4.92	3.91
C18:3n-6	10.02	11.89	8.69
C20:3n-6	(1.28%)* 0.13	(11.1%)* 1.48	(19.4%)* 2.09
C20:4n-6	46.98	28.87	35.25
C22:4n-6	0	0	0
Total lipid (mg)	212	174	187
*% conversion=product/(substrate+product)			

Figure 49

1	ATGAACATGT	CAGTGTGAC	TTTACAAGAA	TATGAATTCG	AAAAGCAGTT
51	CAACGAGAAT	GAAGCCATCC	AATGGATGCA	GGAAAACCTGG	AAGAAATCTT
101	TCCTGTTTTT	TGCTCTGTAT	GCTGCCTTTA	TATTCGGTGG	TCGGCACCTA
151	ATGAATAAAC	GAGCAAAGTT	TGAACTGAGG	AAGCCATTAG	TGCTCTGGTC
201	TCTGACCCTT	GCAGTCTTCA	GTATATTCGG	TGCTCTTCGA	ACTGGTGCTT
251	ATATGGTGTA	CATTTTGTATG	ACCAAAGGCC	TGAAGCAGTC	AGTTTGTGAC
301	CAGGGTTTTT	ACAATGGACC	TGTCAGCAAA	TTCTGGGCTT	ATGCATTTGT
351	GCTAAGCAAA	GCACCCGAAC	TAGGAGATAC	AATATTCATT	ATTCTGAGGA
401	AGCAGAAGCT	GATCTTCCTG	CACTGGTATC	ACCACATCAC	TGTGCTCCTG
451	TACTCTTGGT	ACTCCTACAA	AGACATGGTT	GCCGGGGGAG	GTTGGTTCAT
501	GACTATGAAC	TATGGCGTGC	ACGCCGTGAT	GTACTCTTAC	TATGCCTTGC
551	GGGCGGCAGG	TTTCCGAGTC	TCCCGGAAGT	TTGCCATGTT	CATCACCTTG
601	TCCCAGATCA	CTCAGATGCT	GATGGGCTGT	GTGGTTAACT	ACCTGGTCTT
651	CTGCTGGATG	CAGCATGACC	AGTGTCACCTC	TCACTTTCAG	AACATCTTCT
701	GGTCCTCACT	CATGTACCTC	AGCTACCTTG	TGCTCTTCTG	CCATTTCTTC
751	TTTGAGGCCT	ACATCGGCAA	AATGAGGAAA	ACAACGAAAG	CTGAATAG

Figure 50

1 MNMSVLTQLQE YEFKQFNEN EAIQWMQENW KKSFLFSALY AAFIFGGRHL
51 MNKRAKFELR KPLVLWSTL AVFSIFGALR TGAYMVYILM TKGLKQSVCD
101 QGFYNGPVSK FWAYAFVLSK APELGDITFI ILRKQKLIFL HWYHHITVLL
151 YSWYSYKDMV AGGGWFMTMN YGVHAVMYSY YALRAAGFRV SRKFAMFITL
201 SQITQMLMGC VVNYLVFCWM QHDQCHSHFQ NIFWSSLMYL SYLVLFCHFF
251 FEAYIGEMRK TTKAE*

Figure 51

Host	334	334	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58
Substrate	GLA	GLA	AA	AA	STA	STA	EPA	EPA	OA	OA	ALA	ALA	ALA	ALA
Concentration	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM
% total lipid														
C18:1n-9	18.75	12.96	16.95	12.76	16.06	14.48	19.55	13.78	29.42	23.06	ND	14.58		
C18:1n-7	2.00	18.49	2.30	18.70	1.45	13.26	2.75	13.62	2.50	16.42	1.87	13.76		
C18:1n-5	0.29	1.63	0.24	1.61	0.33	0.97	0.32	1.10	0.30	1.64	0.28	1.18		
C18:3n-6	4.61	2.02	0.04	0.04	0.02	0.09	0.06	0.05	0.02	0.05	0.01	0.01		
C18:3n-3	0.02	0.08	0.02	0.07	0.01	0.03	0.04	0.05	0.02	0.08	14.74	14.08		
C18:4n-3	ND	ND	ND	ND	7.01	2.65	ND	ND	ND	ND	ND	ND		
C20:1n-9	0.10	0.77	0.11	0.70	0.15	0.55	0.15	0.46	0.27	2.25	0.10	0.57		
C20:1n-7	0.08	8.45	0.10	8.06	0.04	3.95	0.14	4.48	0.10	(8.9%/9.35)	0.06	3.53		
C20:3n-6	0.17	(78.3%/7.29)	0.01	0.07	ND	0.04	ND	ND	ND	ND	ND	ND		
C20:3n-3	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	0.41	(30.4%/6.15)		
C20:4n-6	ND	ND	22.07	8.40	ND	0.07	ND	ND	ND	ND	ND	ND		
C20:4n-3	ND	ND	ND	ND	0.25	(79.2%/10.07)	ND	ND	ND	ND	ND	ND		
C20:5n-3	ND	ND	0.01	ND	0.18	0.08	8.21	2.63	ND	0.02	ND	ND		
C22:4n-6	ND	ND	ND	(42.7%/6.26)	ND	ND	ND	ND	ND	ND	ND	ND		
C22:5n-3	ND	ND	ND	ND	ND	0.18	ND	ND	ND	ND	ND	ND		
Total Lipid	158	104	144	112	324	209	178	94	148	87	243	315		

(% conversion) = product/(substrate + product)
 ND= not detected

Figure 52

Host	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	pRAE-58
Substrate	GLA	GLA	GLA	GLA	AA	AA	AA	AA	AA	AA	AA	EPA	EPA	EPA	EPA	EPA	EPA	EPA	EPA
Concentration	25μM	25μM	100μM	100μM	25μM	25μM	100μM	100μM	25μM	25μM	100μM	100μM	25μM	25μM	100μM	100μM	100μM	100μM	100μM
% total lipid																			
C18:1n-9	23.82	21.49	18.49	17.41	22.09	19.23	17.45	18.44	24.78	21.28	19.42	18.85							
C18:1n-7	2.52	18.35	1.71	11.82	2.54	18.77	1.78	12.67	2.64	19.48	1.79	12.40							
C18:1n-5	0.15	1.13	0.10	0.54	0.15	1.23	0.10	0.63	0.15	1.18	0.09	0.62							
C18:3n-6	6.10	2.38	23.30	14.46	0.04	0.02	0.04	0.02	0.04	0.02	0.01	0.01							
C20:1n-9	0.08	0.83	0.05	0.48	0.10	1.18	0.04	0.56	0.10	1.30	0.06	0.63							
C20:1n-7	0.10	5.75	0.07	3.09	0.11	9.49	0.05	3.62	0.10	9.94	0.08	4.07							
C20:3n-6	0.15	(62.4%)3.95	0.31	(39.8%)9.56	0.02	ND	ND	0.04	ND	0.02	0.01	0.01							
C20:4n-6	ND	ND	0.01	ND	11.76	7.68	28.39	21.02	0.02	0.02	ND	0.01							
C20:5n-3	ND	ND	ND	ND	0.03	0.02	0.10	0.07	4.79	2.04	26.47	13.69							
C22:4n-6	ND	ND	ND	ND	ND	(27.5%)2.91	0.01	(15.7%)3.90	ND	ND	0.00	ND							
C22:5n-3	ND	ND	ND	ND	ND	ND	ND	0.03	0.02	(70.3%)4.82	0.04	(45.7%)11.50							
Total Lipid	230	419	590	576	249	332	1014	961	372	390	1323	1065							

(% conversion) = product/(substrate + product)
 ND= not detected

Figure 53

A

Host	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242
Substrate	PA	PA	SA	SA	ARA	ARA	BA	BA	PTA	PTA	OA	OA	EA	EA	EA	EA	EA	EA	EA
Concentration	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM
% total lipid																			
C16:0	24.17	17.23	11.22	7.90	7.74	7.98	7.62	7.11	17.28	11.04	16.06	12.76	14.37	11.98					
C16:1n-7	39.83	33.83	30.62	20.56	21.61	19.81	21.34	22.89	50.06	39.43	40.95	30.06	43.34	29.51					
C16:1n-5	0.30	0.74	0.29	0.58	0.17	0.47	0.18	0.59	0.38	0.80	0.34	0.68	0.37	0.71					
C18:0	1.90	1.50	35.82	38.10	1.12	0.89	1.03	0.88	1.90	1.44	1.82	1.43	1.51	1.23					
C18:1n-9	15.36	14.11	11.52	10.88	8.29	10.03	8.09	10.25	14.55	13.86	20.12	21.37	14.12	15.15					
C18:1n-7	1.36	11.44	0.90	8.72	0.69	8.51	0.69	8.58	1.30	12.76	1.30	13.79	1.21	12.66					
C18:1n-5	0.11	0.78	0.08	0.69	0.08	0.54	0.06	0.61	0.19	0.76	0.10	0.90	0.15	0.84					
C20:0	0.15	0.17	0.09	0.12	52.07	41.48	ND	ND	ND	ND	ND	ND	ND	0.17	0.23				
C20:1n-9	0.09	0.45	0.05	0.30	0.03	ND	0.06	0.28	0.05	0.38	0.18	0.58	7.47	10.97					
C20:1n-7	0.20	2.84	ND	1.52	0.05	1.43	0.14	1.60	0.07	2.76	0.12	2.08	ND	2.30					
C22:0	0.43	0.56	0.29	0.22	0.31	0.19	52.91	38.43	ND	ND	ND	ND	ND	0.32					
C24:0	0.59	1.39	0.36	0.85	0.45	0.71	0.53	1.14	0.45	1.63	0.66	1.02	0.56	0.79					
Total Lipid	297	272	573	542	558	846	585	519	464	295	306	448	309	648					

ND = not detected

Figure 53

B

Host	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58
Substrate	LA	LA	GLA	GLA	DGLA	DGLA	AA	AA	ADA	ADA
Concentration	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM
	% total lipid									
C18:1n-9	15.27	16.83	14.85	15.58	13.62	16.24	15.08	15.64	16.18	13.98
C18:1n-7	1.21	13.53	1.22	11.80	1.16	12.63	1.18	11.70	1.30	10.67
C18:1n-5	0.13	0.95	0.20	0.73	0.12	0.72	0.14	0.59	0.12	0.70
C18:2n-6	4.09	4.85	0.09	0.07	0.07	0.04	0.04	0.04	0.03	0.07
C18:3n-6	ND	ND	4.66	2.33	ND	ND	ND	ND	ND	ND
C20:1n-9	0.07	2.60	0.07	0.33	0.07	0.33	0.04	0.27	0.08	0.33
C20:1n-7	0.10	0.18	0.14	1.65	0.08	1.68	0.12	1.58	0.12	1.85
C20:2n-6	ND	(13.2%)0.74	ND	ND	ND	ND	ND	ND	ND	ND
C20:3n-6	ND	ND	ND	(51.4%)2.46	6.37	7.86	ND	0.03	ND	ND
C20:4n-6	ND	ND	ND	ND	ND	0.09	6.49	5.77	ND	ND
C22:4n-6	ND	ND	ND	ND	ND	ND	ND	(27.1%)2.14	10.91	15.57
C24:0	0.59	1.61	0.64	1.12	0.69	0.79	0.52	0.77	0.54	1.26
Total Lipid	333	373	260	392	260	672	553	690	706	440

C

Host	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58
Substrate	ALA	ALA	STA	STA	EPA	EPA	DPA	DPA		
Concentration	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM		
	% total lipid									
C18:1n-9	17.21	17.36	16.85	17.71	16.45	16.93	17.08	16.68	18.36	18.77
C18:1n-7	1.29	12.20	1.15	11.38	1.23	11.48	1.33	11.61	1.46	13.72
C18:1n-5	0.14	0.68	0.12	0.57	0.12	0.54	0.12	0.63	0.13	0.79
C18:3n-3	4.42	3.61	ND	0.03	ND	0.03	ND	0.03	ND	0.03
C18:4n-3	ND	0.13	3.04	1.38	ND	0.13	ND	0.13	ND	0.17
C20:1n-9	0.09	0.33	0.11	0.34	0.05	0.31	0.09	0.30	0.13	0.34
C20:1n-7	0.13	1.55	0.05	1.38	0.23	1.89	0.18	1.73	0.15	1.76
C20:3n-3	0.06	(22.2%)1.03	ND	ND	ND	0.11	ND	ND	ND	ND
C20:4n-3	ND	ND	0.06	(61.9%)2.24	ND	ND	ND	ND	ND	ND
C20:5n-3	ND	ND	0.05	0.05	7.43	4.88	ND	ND	0.07	ND
C22:4n-3	ND	ND	ND	0.39	ND	ND	ND	ND	ND	ND
C22:5n-6	ND	ND	ND	ND	ND	ND	0.28	0.41	ND	ND
C22:5n-3	ND	ND	ND	ND	ND	(39.5%)3.19	3.99	5.94	ND	ND
C24:0	0.43	0.73	0.33	0.73	0.45	0.84	0.64	1.07	0.68	0.77
C24:5n-3	ND	ND	ND	ND	ND	0.08	ND	0.06		ND
Total Lipid	696	729	911	710	719	703	602	642	397	684

(% conversion) = product/(substrate + product)

ND= not detected

Figure 54

```
1  ATGGAGCAGC TGAAGGCCTT TGATAATGAA GTCAATGCTT TCTTGGACAA
51 CATGTTTGGG CCACGAGATT CTCGAGTTCG CGGGTGGTTC CTGCTGGACT
101 CTTACCTTCC CACCTTCATC CTCACCATCA CGTACCTGCT CTCGATATGG
151 CTGGGTAACA AGTACATGAA GAACAGGCCT GCTCTGTCTC TCAGGGGCAT
201 CCTCACCTTG TATAACCTCG CAATCACACT TCTTTCTGCG TATATGCTGG
251 TGGAGCTCAT CCTCTCCAGC TGGGAAGGAG GTTACAACCT GCAGTGTGAG
301 AATCTCGACA GTGCAGGAGA AGGTGATGTC CGGGTAGCCA AGGTCTTGTG
351 GTGGTACTAC TTCTCCAAAC TAGTGGAGTT CCTGGACACG ATTTTCTTTG
401 TTCTACGAAA AAAGACCAAT CAGATCACCT TCCTTCATGT CTATCACCAC
451 GCGTCCATGT TCAACATCTG GTGGTGTGTT TTGAACTGGA TACCTTGTGG
501 TCAAAGCTTC TTTGGACCCA CCCTGAACAG CTTTATCCAC ATTCTCATGT
551 ACTCCTACTA CGGCCTGTCT GTGTTCCCGT CCATGCACAA GTACCTTTGG
601 TGGAAGAAGT ACCTCACACA GGCTCAGCTG GTGCAGTTCG TACTCACCAT
651 CACGCACACG CTGAGTGCCG TGGTGAAGCC CTGTGGCTTC CCCTTTGGCT
701 GTCTCATCTT CCAGTCTTCC TATATGATGA CGCTGGTCAT CCTGTTCTTA
751 AACTTCTATA TTCAGACATA CCGGAAAAAG CCAGTGAAGA AAGAGCTGCA
801 AGAGAAAGAA GTGAAGAATG GTTTCCCCAA AGCCCACTTA ATTGTGGCTA
851 ATGGCATGAC GGACAAGAAG GCTCAATAA
```


Figure 55

1 MEQLKAFDNE VNAFLDNMFG PRDSRVRGWF LLDSYLPTEI LTITYLLSIW
51 LGNKYMKNRP ALSLRGILT YNLAITLLSA YMLVELILSS WEGGYNLQCQ
101 NLDSAGEGDV RVAKVLWWYY FSKLVEFLDT IFFVLRKKTN QITFLHVVHH
151 ASMFNIWWCV LNWIPCGQSF FGPTLNSFIH ILMYSYYGLS VFPSMHKYLW
201 WKKYLTQAQL VQFVLTITHT LSAVVKPCGF PFGCLIFQSS YMMTLVILFL
251 NFYIQTYRKK PVKKELQEKE VKNGFPAHL IVANGMTDKK AQ*

Figure 56

Host	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242
Substrate	GLA	GLA	AA	AA	ADA	ADA	ADA	STA	STA	EPA	EPA	DPA	DPA	DPA	DPA	DPA	DPA	DPA	DPA
Concentration	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM
% total lipid																			
C18:1n-9	15.94	14.16	12.30	15.67	11.77	11.41	14.81	17.92	15.91	16.33	15.04	14.63							
C18:1n-7	1.25	1.21	1.10	1.50	1.13	1.18	1.19	1.38	1.33	1.49	1.37	1.38							
C18:3n-6	4.53	4.21	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND							
C18:4n-3	ND	ND	ND	ND	ND	ND	2.78	2.70	ND	ND	ND	ND							
C20:1n-7	ND	ND	ND	ND	ND	0.32	ND	0.03	ND	0.05	ND	ND							
C20:3n-6	0.10	0.37	ND	ND	ND	ND	ND	0.05	ND	ND	ND	ND							
C20:4n-6	ND	ND	11.44	5.55	ND	ND	ND	ND	ND	ND	ND	ND							
C20:4n-3	ND	ND	ND	ND	ND	ND	ND	(14%)0.44	ND	ND	ND	ND							
C20:5n-3	ND	ND	ND	ND	ND	ND	ND	9.68	3.02	ND	ND	ND							
C22:4n-6	ND	ND	ND	(10.4%)0.64	20.41	23.61	ND	ND	ND	ND	ND	ND							
C22:4n-3	ND	ND	ND	ND	ND	ND	(42.3%)0.33	ND	ND	ND	0.57	0.57							
C22:5n-3	ND	ND	ND	ND	ND	ND	ND	ND	ND	(32.7%)1.47	7.87	4.88							
C24:4n-6	ND	ND	ND	(62.6%)1.07	ND	(9.2%)2.4	ND	ND	ND	ND	ND	ND							
C24:5n-3	ND	ND	ND	ND	ND	ND	ND	ND	(82.8%)7.06	ND	(43.9%)3.82								
Total Lipid	208	126	115	189	158	149	124	433	221	271	127	126							

(% conversion) = product/(substrate + product)
 ND = not detected

Figure 57

A

Host	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	PYX242	PRAE-84	PYX242	PRAE-84	PYX242	PRAE-84	PYX242	PRAE-84	PYX242	PRAE-84	PYX242	PRAE-84	PYX242	PRAE-84	PYX242	PRAE-84	PYX242	PRAE-84	PYX242
Substrate	PA	PA	SA	SA	ARA	ARA	BA	BA	PTA	PTA	OA	OA	EA	EA	EA	EA	EA	EA	EA
Concentration	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM
% total lipid																			
C16:0	36.30	39.95	7.12	8.31	5.78	4.42	4.17	5.76	18.69	18.85	14.69	18.91	15.25	18.88					
C16:1n-7	26.22	23.52	11.77	15.25	10.23	6.29	7.01	10.10	38.48	41.23	20.55	31.48	25.89	40.32					
C16:1n-5	0.23	0.28	0.16	0.20	0.13	0.07	0.09	0.13	0.38	0.38	0.26	0.43	0.35	0.41					
C18:0	2.26	2.14	64.90	58.73	0.94	1.01	0.64	0.85	2.17	2.29	3.02	2.73	2.71	2.15					
C18:1n-9	14.83	11.27	6.35	7.22	5.20	4.33	3.84	5.12	14.25	14.27	18.44	22.20	14.62	16.91					
C18:1n-7	1.44	1.36	0.57	0.73	0.54	0.51	0.41	0.56	1.57	1.68	1.53	1.67	1.65	1.84					
C18:1n-5	0.10	ND	ND	0.06	ND	ND	ND	0.06	0.17	0.15	ND	0.18	ND	0.16					
C20:0	0.59	0.24	0.09	0.08	66.40	74.78	0.10	0.05	0.17	0.17	0.24	0.20	0.33	0.04					
C20:1n-9	0.06	0.10	ND	0.04	0.05	0.06	ND	ND	ND	ND	0.25	0.16	13.15	7.07					
C20:1n-7	0.07	ND	ND	ND	ND	0.12	ND	ND	ND	ND	0.40	ND	ND	0.04					
C22:0	0.45	0.75	0.29	0.30	0.43	0.31	77.35	70.71	0.74	0.80	0.98	0.74	0.83	0.44					
C24:0	0.55	1.09	0.38	0.41	0.69	0.62	0.50	0.45	0.94	0.92	1.67	0.96	ND	0.53					
Total Lipid	158	104	144	112	324	209	178	94	148	87	243	315	70	529					

ND = not detected

Figure 57

B

Host	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84
Substrate	LA	LA	GLA	GLA	DGLA	DGLA	AA	AA	ADA	ADA
Concentration	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM
% total lipid										
C18:1n-9	12.30	16.12	15.63	16.28	14.28	13.77	16.21	15.04	15.38	12.94
C18:1n-7	1.34	1.87	1.69	1.90	1.41	1.61	1.61	1.62	1.51	1.47
C18:2n-6	2.67	3.61	0.17	0.20	0.24	0.21	0.09	0.09	0.06	0.14
C18:3n-6	ND	ND	2.03	2.49	ND	ND	ND	ND	ND	ND
C20:3n-6	ND	ND	ND	(14.7%)0.43	10.59	10.73	ND	ND	ND	ND
C20:4n-6	ND	ND	ND	ND	ND	ND	14.03	5.27	ND	ND
C22:4n-6	ND	ND	ND	ND	ND	ND	ND	(8.7%) 0.5	11.44	16.60
C24:0	0.79	1.00	1.08	1.16	1.30	0.87	0.87	0.72	0.77	1.18
C24:4n-6	ND	ND	ND	ND	ND	ND	ND	(43.8%)0.39	ND	(7.3%)1.3
C24:5n-6	ND	ND	ND	ND	ND	ND	ND	0.38	ND	ND
Total Lipid	85	87	88	79	107	98	208	212	304	122

C

Host	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84
Substrate	ALA	ALA	STA	STA	EPA	EPA	DPA	DPA		
Concentration	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM		
% total lipid										
C18:1n-9	16.69	16.38	18.24	15.95	14.07	15.16	16.05	15.06	17.47	17.15
C18:1n-7	1.37	1.43	1.71	1.40	1.37	1.47	1.67	1.51	1.75	1.73
C18:2n-6	0.08	0.08	0.12	0.04	0.13	0.06	0.11	0.18	0.13	0.15
C18:3n-3	4.47	4.28	ND	ND	ND	ND	ND	ND	ND	ND
C18:4n-3	ND	ND	2.28	2.39	ND	ND	ND	ND	ND	ND
C20:3n-3	(1.3%)0.06	(3.6%)0.16	ND	ND	ND	0.26	ND	ND	ND	0.12
C20:4n-3	ND	ND	ND	(11.1%)0.3	ND	ND	ND	ND	ND	ND
C20:5n-3	ND	0.07	ND	ND	9.97	3.84	ND	ND	ND	ND
C22:4n-3	ND	ND	ND	(43.4%)0.23	ND	ND	ND	ND	ND	ND
C22:5n-6	ND	ND	ND	ND	ND	ND	0.64	0.55	ND	ND
C22:5n-3	ND	ND	ND	ND	ND	(24.0%)1.21	8.79	3.57	ND	ND
C24:0	0.65	0.43	1.41	0.58	1.38	0.78	1.45	1.35	0.89	0.67
C24:5n-3	ND	ND	ND	ND	ND	(73.6%)3.38	ND	(46.4%)3.09	ND	ND
Total Lipid	362	384	173	393	124	280	137	151	190	200

*% conversion = product/(substrate + product)

ND= not detected

Figure 58

1	ATGGAACATT	TCGATGCGTC	ACTCAGTACC	TATTTCAAGG	CCTTCCTGGG
51	CCCCCGAGAT	ACAAGAGTCA	AAGGATGGTT	CCTCCTGGAC	AATTACATCC
101	CTACGTTTGT	CTGTTCTGTT	ATTTACTTAC	TCATTGTATG	GCTGGGACCA
151	AAATACATGA	AGAACCGGCA	GCCGTTCTCT	TGCCGAGGCA	TCCTGCAGTT
201	GTATAACCTT	GGACTCACCC	TGCTGTCTCT	CTACATGTTT	TATGAGTTGG
251	TGACAGGTGT	GTGGGAGGGC	AAATACAAC	TTTTCTGCCA	GGGAACACGC
301	AGCGCGGGAG	AATCCGATAT	GAAGATCATC	CGCGTCCTCT	GGTGGTACTA
351	CTTCTCCAAA	CTCATCGAAT	TCATGGACAC	CTTTTTCTTC	ATCCTTCGCA
401	AGAACAACCA	CCAGATCACC	GTGCTCCATG	TCTACCACCA	CGCTACCATG
451	CTCAACATCT	GGTGGTTTGT	GATGAACTGG	GTTCCCTGCG	GCCATTCATA
501	TTTTGGTGCG	ACACTCAACA	GCTTCATCCA	TGTCCTCATG	TACTCGTACT
551	ATGGTCTGTC	CTCCATCCCG	TCCATGCGTC	CCTACCTCTG	GTGGAAAAAG
601	TACATCACTC	AAGGGCAGCT	GGTCCAGTTT	GTGCTGACAA	TCATCCAGAC
651	GACCTGCGGG	GTCTTCTGGC	CATGCTCCTT	CCCTCTCGGG	TGGCTGTTCT
701	TCCAGATTGG	ATACATGATT	TCCCTGATTG	CTCTCTTCAC	AAACTTCTAC
751	ATTCAGACTT	ACAACAAGAA	AGGGGCCTCT	CGGAGGAAAG	ACCACCTGAA
801	GGGCCACCAG	AACGGGTCTG	TGGCCGCCGT	CAACGGACAC	ACCAACAGCT
851	TCCCTTCCCT	GGAAAACAGC	GTGAAGCCCA	GGAAGCAGCG	AAAGGATTGA

Figure 59

1 MEHFDASLST YFKAFLGPRD TRVKGWFLLD NYIPTFVCSV IYLLIVWLGP
51 KYMKNRQPFS CRGILQLYNL GLTLLSLYMF YELVTGVWEG KYNFFCQGTR
101 SAGESDMKII RVLWWYYFSK LIEFMDTFFF ILRKNNHQIT VLHVVYHHATM
151 LNIWWFVMNW VPCGHSYFGA TLNSFIHVLM YSYYGLSSIP SMRPYLWWKK
201 YITQGQLVQF VLTIIQTTCG VFWPCSFPLG WLFFQIGYMI SLIALFTNFI
251 IQTYNKKGAS RRDHLLKGHQ NGSVAAVNGH TNSFPSELS VKPRKQRKD*

Figure 60

[illegible]
$$(\% \text{ conversion}) = \text{product} / (\text{substrate} + \text{product})$$

ND = not detected

Figure 61

Host (plasmid)	334(pYX242)	334(pRET-22)	334(pYX242)	334(pRET-22)	334(pYX242)	334(pRET-22)
Added Substrates	50 mM GLA	50 mM GLA	50 mM AA	50 mM AA	no substrate	no substrate
Fatty Acid	%total lipid					
C16:0	19.8	18.59	13.8	6.23	13.62	13.63
C16:1n-7	20.92	17.74	26.62	13.01	40.1	47.67
C18:0	5.79	4.94	3.62	2	4.86	5.031
C18:1n-7	(3.9%) 0.85	(9.12%) 1.78	(3.5%) 0.97	(12.54%) 1.18	(3.6%) 1.5	(7.53%) 3.88
C18:1n-9	8.46	7.45	10.27	5.36	13.7	16.93
C18:3n-6	*26.62	*22.03	0.03	0.01		
C20:3n-6	(1.1%) 0.3	(38.2%) 13.61				
C20:4n-6			*27.36	*65.38		
C22:4n-6						
Total lipid (μg)	36	42	85	280	55	79
(% conversion)=product/(substrate+product)						

*indicates substrate added

Figure 62

A.

Host(plasmid)	334(pRET22)	334(pRET22)	334(pRET22)	334(pRET22)	334(pRET22)	334(pRET22)	334(pRET22)
Added substrate	50 μ M SA C18:0	50 μ M OA C18:1n-9	50 μ M LA C18:2n-6	50 μ M DGLA C20:3n-6	25 μ M AA C20:4n-6	50 μ M Adrenic C22:4n-6	
Fatty Acid	% total lipid						
C16:0	12.9	12.54	15.23	9.1	10.2	3.42	
C16:1	37.71	23.83	24.87	16.61	18.375	7.66	
C18:0	11.44	4.7	4.49	2.7	2.9	1.23	
C18:1n-9	14.03	*16.87	9.54	6.74	6.39	2.99	
C18:2n-6			16.87	0.15		0.28	
C18:3n-6							
C20:2n-6						0.05	
C20:3n-6							
C20:4n-6							
C22:4n-6							
Total Lipid (μ g)	63	103	71	110	97	277	

B.

Host(plasmid)	334(pRET22)	334(pRET22)	334(pRET22)	334(pRET22)
Added substrate	50 μ M ALA C18:3n-3	50 μ M PA C18:0	50 μ M EPA C20:5n-3	50 μ M STA C18:4n-3
Fatty Acid	% total lipid			
C16:0	13.91	15.06	16.92	20.08
C16:1	14.74	31.77	23.57	20.17
C18:0	4.06	*4.85	4.94	6.02
C18:1n-9	6.65	13.59	10.46	9.29
C18:3n-3	*38.66			
C18:4n-3				*20.45
C20:4n-3				(12.57%) 2.94
C22:5n-3			*15.48	
Total Lipid (μ g)	80	84	81	60

* indicates substrate added
(% conversion) = product/(substrate+product)

Figure 63

A.

Host(plasmid)	334(pRET-22+pCGR-4)	334(pYX242+pYES2)
Addc substrate	50μM GLA	50μM GLA
Fatty Acid	% total lipid	
C16:0	15.92	15.07
C16:1n-7	24.97	19.48
C18:0	8.52	6.48
C18:1n-7	3.9	1.61
C18:1n-9	18.48	12.71
C18:3n-6	*7.0	*10.54
C20:0	0	0
C20:3n-6	(27.81%) 4.36	(1.58%) 0.17
C20:4n-6	(27.55%) 4.32	0
Total Lipid (μg)	508	168

B.

Host(plasmid)	334(pRET-22+pCGR-4)	334(pYX242+pYES2)
Addc substrate	50μM STA	50μM STA
Fatty Acid	% total lipid	
C16:0	18.74	16.21
C16:1n-7	21.35	26.09
C18:0	6.78	7.57
C18:1n-7	1.97	1.7
C18:1n-9	20.73	22.41
C18:4n-3	*6.05	*13.43
C20:0	0	0.45
C20:4n-3	(15.88%) 1.68	(4.73%) 0.69
C20:5n-3	(26.93%) 2.85	(3.22%) 0.47
Total Lipid (μg)	335	161

* indicates substrate added
(% conversion) = product/(substrate+product)